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### On protein - protein search, using sw model

Run on: March 19, 2003, 12:06:07 ; Search time 36 Seconds  
 (without alignments)  
 103.639 Million cell updates/sec

Title: US-09-508-083-1

Perfect score: 144

Sequence:

1 HARCTFTSDVSSYLEQQAKEFIWALVK 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:  
 Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A\_Geneseq\_101002:\*

- 1: /SIDS1/gcadata/geneseq/geneseq-emb1/AA1986.DAT:\*
- 2: /SIDS1/gcadata/geneseq/geneseq-emb1/AA1981.DAT:\*
- 3: /SIDS1/gcadata/geneseq/geneseq-emb1/AA1982.DAT:\*
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- 14: /SIDS1/gcadata/geneseq/geneseq-emb1/AA1993.DAT:\*
- 15: /SIDS1/gcadata/geneseq/geneseq-emb1/AA1994.DAT:\*
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- 19: /SIDS1/gcadata/geneseq/geneseq-emb1/AA1998.DAT:\*
- 20: /SIDS1/gcadata/geneseq/geneseq-emb1/AA1999.DAT:\*
- 21: /SIDS1/gcadata/geneseq/geneseq-emb1/AA2000.DAT:\*
- 22: /SIDS1/gcadata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SIDS1/gcadata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	144	100.0	28 15 AAR45427	Insulinotropin derivative
2	144	100.0	28 15 AAR63249	Insulinotropin (GL)
3	144	100.0	28 17 AAW16659	Tetradecanoylated
4	144	100.0	28 17 AAW02654	Glucagon-like pept.
5	144	100.0	28 17 AAR9850	Target peptide (GL)
6	144	100.0	28 20 AAW93527	Peptide used in tr
7	144	100.0	28 21 RAB70295	Modified Glucagon
8	144	100.0	28 21 AAY78952	Glucagon-like pept.
9	144	100.0	28 22 AAE09256	Human glucagon-like
10	144	100.0	28 22 AAG63270	Amino acid sequenc

### ALIGNMENTS

#### RESULT 1

ID AAR45437 standard; protein: 28 AA.  
 XX  
 AC AAR45437;

DT 27-JUN-1994 (first entry)  
 XX  
 DE Insulinotropin derivative.

XX  
 KW Insulinotropic; activity; enhancing insulin activity; treatment;  
 KW Type II diabetes.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9325579-A.  
 XX  
 PD 23-DEC-1993.

XX  
 PR 14-APR-1993; 93WO-US033988.  
 XX  
 PR 15-JUN-1992; 92US-0899073.  
 XX  
 PA (PFIZER ) PFIZER INC.  
 XX  
 PI Andrews GC, Daunay GO, Francoeur ML, Larson ER;  
 XX  
 DR WPI; 1994-007457/01.  
 XX  
 PT New derivs. of glucagon-like peptide 1 and insulinotropin - used for  
 PT enhancing insulin action in a mammal, partic. by iontophoretic admin.  
 XX  
 PS Claim 3; Page 20; 32pp; English.

XX The sequence is that of a derivative of insulinotropin which  
 CC has insulinotropic activity and is useful for enhancing insulin  
 CC action in a mammal, partic. for treating Type II diabetes  
 CC (claimed). It is partic. suited for delivery to a mammal by  
 CC ionophoresis.  
 XX Sequence 28 AA;  
 SQ RESULT 2  
 Query Match 100.0%; Score 144; DB 15; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-14; Mismatches 0;  
 Matches 28; Conservative 0; Indels 0; Gaps 0;  
 ID 1 HAEGTFTSDVSSYLEGQAAKEFIAWLVK 28  
 Db 1 HAEGTFTSDVSSYLEGQAAKEFIAWLVK 28  
 DE 1 HAEGTFTSDVSSYLEGQAAKEFIAWLVK 28  
 DT 22-JUL-1997 (first entry)  
 XX AAR63249 standard; peptide; 28 AA.  
 XX AAR63249;  
 XX DT 02-MAY-1995 (first entry)  
 DE Insulinotropin (GLP-1(7-34)) for use in treating NIDDM.  
 XX KW insulinotropic activity; GLP-1; glucagon-like protein 1; NIDDM;  
 KW non-insulin dependent diabetes mellitus; insulinotropin; truncated.  
 XX OS Synthetic.  
 XX PR EP619322-A.  
 XX PD 12-OCT-1994.  
 XX PF 10-FEB-1994; 94EP-0300981.  
 XX - 07-APR-1993; 930S-0044133.  
 XX PA (PFIZER ) PFIZER INC.  
 XX PA (PFIZER ) PFIZER CORP.  
 PI Danley DE, Gelfand RA, Geoghegan KE, Kim Y, Lambert WJ;  
 PI QI H, Oh, Hong Q, Yesook K;  
 XX WPI: 1994-31174/39.  
 XX PT treatment of non-insulin dependent diabetes mellitus - using a  
 PT glucagon-like peptide 1 or deriv. with prolonged action for  
 PT sustained glycaemic control  
 XX PS Claim 2: Page 46; 70pp; English.  
 XX This peptide is GLP-1(7-34) [GLP = glucagon-like peptide], a truncated  
 CC deriv. of GLP-1. GLP-1 and its deriv.s are useful in the treatment of  
 CC Non-Insulin Dependent Diabetes Mellitus (NIDDM). During processing in  
 CC the pancreas and intestine, GLP-1 (AAR63245) is converted to a 31 amino  
 CC acid peptide having amino acids 7-37 of GLP-1, alternatively referred  
 CC to as insulinotropin. GLP-1(7-37) has insulinotropic activity, ie. it  
 CC is able to stimulate, or cause to be stimulated, the synthesis of the  
 hormone insulin. Other derivs. of GLP-1 are shown in AAR6346-51. It  
 CC has been discovered that prolonged plasma elevations of GLP-1, and  
 CC related polypeptides, are necessary during the meal and beyond to  
 CC achieve sustained glycemic control in patients w/ NIDDM. The invention  
 CC provides a compsn. that has prolonged action after each administration.  
 XX Sequence 28 AA;  
 SQ RESULT 3  
 Query Match 100.0%; Score 144; DB 15; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-14; Mismatches 0;  
 Matches 28; Conservative 0; Indels 0; Gaps 0;  
 ID 1 HAEGTFTSDVSSYLEGQAAKEFIAWLVK 28  
 AC AAW16669;  
 XX DT 22-JUL-1997 (first entry)  
 XX AAW16669 standard; peptide; 28 AA.  
 XX AAW16669;  
 DE Tetradecanoylated glucagon like peptide 1 derivative.  
 XX KW Hormone; derivative; glucagon like peptide 1; modification;  
 KW lipophilic substituent; tetradecanoyl; protracted; action;  
 KW profile; GLP-1.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT Modified-site 28  
 FT /notes="Lys Nepsilon-Lys-Nalpha-tetradecanoyl  
 FT -OH]-COOH"  
 XX PN WO9629342-A1.  
 XX PD 26-SEP-1996.  
 XX PF 18-MAR-1996; 96WO-DK00105.  
 XX PR 17-MAR-1995; 95DK-0000275.  
 XX PA (NOVO ) NOVO-NORDISK AS.  
 XX PT Halstrom JB, Hansen PH, Havelund S, Jonassen I;  
 PI Kurtzhals P;  
 XX DR WPI: 1996-443133/44.  
 XX PT New peptide hormone derivs. - having a lipophilic substt.  
 PT introduced into the N-terminal or C-terminal for a protracted  
 PT profile of action.  
 XX PS Disclosure; Page 5; 21pp; English.  
 XX The present sequence is a pharmacologically active peptide hormone  
 CC (PT) derivitive, where the parent PH, glucagon like peptide 1,  
 CC has been modified by introducing a carboxy-terminal lipophilic  
 CC substituent, specifically tetradecanoyl, giving it a protracted  
 CC profile of action in the body compared to the parent PH.  
 XX SQ Sequence 28 AA;  
 Query Match 100.0%; Score 144; DB 17; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-14; Mismatches 0;  
 Matches 28; Conservative 0; Indels 0; Gaps 0;  
 ID 1 HAEGTFTSDVSSYLEGQAAKEFIAWLVK 28  
 Db 1 HAEGTFTSDVSSYLEGQAAKEFIAWLVK 28  
 DE 24-JAN-1997 (first entry)  
 XX AAW02644 standard; Peptide; 28 AA.  
 AC AAW02644;  
 XX DT 24-JAN-1997 (first entry)

Query Match 100.0%; Score 144; DB 15; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-14; Mismatches 0;  
 Matches 28; Conservative 0; Indels 0; Gaps 0;

DE Glucagon-like peptide-1 residues 7-34.

XX KW GLP-1 (7-34); thirotropic; insulinotropic; diabetes; treatment;

KW phenol; alcohol; aromatic; gel; protracted release.

XX OS Synthetic.

XX PN WO962005-A1.

XX PD 04-JUL-1996.

XX PF 21-DEC-1995; 95WO-DK00516.

XX PR 23-DEC-1994; 94DK-0001478.

XX PA (NOVO ) NOVO-NORDISK AS.

XX PT JENSEN E, Jorgensen KH;

XX DR WPI; 1996-321644/32.

XX PT New compns, contg. glucagon-like peptide-1 - comprising gels for

PT the protracted released of GLP-1 in the treatment of diabetes mellitus.

XX PS Disclosure; Page 3; 16pp; English.

CC The present sequence is that of residues 7-34 of glucagon-like peptide-1

CC (GLP-1 (7-34)). Compns, contg. a GLP-1 cpd. and a phenolic and/or an

CC . alcoholic aromatic cpd. result in a thirotropic gel showing a protracted

CC release of the active GLP-1 cpd. The compns. can be used as

CC insulinotropic agents in the treatment of diabetes. In partic. GLP-1

CC (7-37) is used in the examples of the invention (sequence not given).

XX SQ : Sequence 28 AA:

Query Match 100.0%; score 144; DB 17; Length 28;

Best Local Similarity 100.0%; Pred. No. 2.1e-14; Mismatches 0; Indels 0; Gaps 0;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QV 1 HAEGTFNSDVSSYLEGQAKERIAWLVK 28

DB 1 HAEGTFNSDVSSYLEGQAKERIAWLVK 28

RESULT 5

1 HAEGTFNSDVSSYLEGQAKERIAWLVK 28

AC AAW93527;

XX DT 15-JUN-1999 (first entry)

XX DE Peptide used in treatment of diabetes mellitus and obesity.

XX KW Diabetes mellitus; obesity; therapy; treatment; hormone; cAMP; cGMP;

KW cyclic adenosine monophosphate; cyclic nucleotide degradation;

KW cyclic guanosine monophosphate; antidiabetic; hypoglycaemic; acromegaly;

KW anti-obesity; non-insulin dependent; mature onset; pancreatectomy; pheochromocytoma;

KW secondary hyperglycemia; pancreatitis; pancreatic disease; hemochromatosis; endocrine disease; Cushing's syndrome; iatrogenic;

KW hyperthyroidism; benzothiadiazine saluretic; diazoxide; glucocorticoid;

KW pathological glucose tolerance; hyperglycemia, dyslipoproteinemia; hyperlipoproteinemia; hypertension.

XX OS Synthetic.

XX DE Target peptide (GLP1(7-34)) used in fusion protein construct.

XX KW Fusion protein construct; isolation; purification;

KW growth hormone releasing factor; glucagon-like peptide 1;

KW parathyroid hormone; inclusion body; carbonic anhydrase.

XX OS Synthetic.

XX PN WO9617942-A1.

XX PD 13-JUN-1996.

XX PF 07-DEC-1995; 95WO-US15800.

XX PR 07-DEC-1994; 94US-0350530.

XX PA (BION-) BIORNEBRASKA INC.

XX PI De LA MOTTE RS, Henriksen DB, Holmquist B, Manning SD;

PI Partridge BE, Stout JS, Wagner FW;  
PS Claim 30; Page 18; 38pp; German.

XX DR WPI; 1996-287186/29.

XX PT Isolation and purificn of peptide(s) from fusion protein constructs

PT - which include a carbonic anhydrase and a variable fused

OS polypeptide

XX PS Claim 18; Page 47; 67pp; English.

CC A new method for the isolation and/or purification of a recombinant peptide employs a fusion protein construct (FPC) comprising a carbonic anhydrase and a variable fused polypeptide containing a target peptide. The method comprises precipitating either the FPC or a fragment of the FPC including the carbonic anhydrase. An alternative method of producing the peptide comprises expressing the FPC as part of an inclusion body. The target peptides of the FPC are derived from growth hormone releasing factor (GRF), glucagon-like peptide 1 (GLP1) or parathyroid hormone (PTH). This sequence corresponds to amino acids 7-34 of GLP1.

XX Sequence 28 AA;

Query Match Best Local Similarity 100.0%; Score 144; DB 17; Length 28; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX ID AAW93527 standard; peptide; 28 AA.

XX AC AAW93527;

RESULT 6

XX DT 15-JUN-1999 (first entry)

XX DE Peptide used in treatment of diabetes mellitus and obesity.

XX KW Diabetes mellitus; obesity; therapy; treatment; hormone; cAMP; cGMP;

KW cyclic adenosine monophosphate; cyclic nucleotide degradation;

KW cyclic guanosine monophosphate; antidiabetic; hypoglycaemic; acromegaly;

KW anti-obesity; non-insulin dependent; mature onset; pancreatectomy; pheochromocytoma;

KW secondary hyperglycemia; pancreatitis; pancreatic disease; Cushing's syndrome; iatrogenic;

KW hemochromatosis; endocrine disease; Cushing's syndrome; glucocorticoid;

KW pathological glucose tolerance; hyperglycemia, dyslipoproteinemia; hyperlipoproteinemia; hypertension.

XX OS Synthetic.

XX PN WO9914239-A1.

XX PD 25-MAR-1999.

XX PF 11-SEP-1998; 98WO-EP05804.

XX PR 11-MAR-1998; 98DE-1010515.

PR 12-SEP-1997; 97DE-040081.

PR 23-DEC-1997; 97DE-105739.

XX PA (FORSS-) FORSSMANN W G.

XX PI Adermann K, Forssmann WG, Meyer M, Richter R;

XX DR WPI; 1999-244026/20.

XX PT Composition containing stimulators of cyclic nucleotide

PT monophosphate

XX PS Claim 30; Page 18; 38pp; German.

xx  
 CC This invention describes a composition containing at least two of the  
 CC components (a) hormone that stimulates production of cyclic adenosine  
 CC monophosphate (cAMP); (b) inhibitor of cyclic nucleotide degradation  
 CC and (c) hormone that stimulates production of cyclic guanosine  
 CC monophosphate (cGMP). This composition has antidiabetic, hypoglycaemic,  
 CC and anti-obesity activity. The product described in the invention  
 can be used for treatment of (i) diabetes mellitus (non-)insulin  
 dependent or mature onset diabetes, (ii) secondary hyperglycemia  
 associated with pancreatic disease (chronic pancreatitis, pancreatectomy  
 CC or hemochromatosis), or endocrine disease (acromegaly, Cushing's  
 syndrome, pheochromocytoma or hyperthyreosis), (iii) iatrogenic  
 CC hyperglycemia (e.g. caused by benzothiadiazine saliuretics, diazoxide or  
 CC glucocorticoids), (iv) pathological glucose tolerance, (v) hyperglycemia,  
 CC (vi) dyslipoproteinemia, (vii) obesity, (viii) hyperlipoproteinemia  
 CC and/or hypotension.

SQ Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 20;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

RESULT 7

ID	AAB07295	standard; peptide; 28 AA.
XX	AAB07295;	
XX	- 17-JAN-2001 (first entry)	
DE	Modified Glucagon Like Peptide (GLP) # 5.	
XX	Peptide amidation; C-terminal alpha-carboxamide; GLP; clostripain; - amidative cleavage; clostridopeptidase B; glucagon like peptide.	
OS	Unidentified.	
XX	WO20002B067-A1.	
XX	18-MAY-2000.	
PD		
XX	05-NOV-1999; 99W0-US26060.	
PR	06-NOV-1998; 98US-0107311. 16-DEC-1998; 98US-0212663.	
XX	(BION-) BIONEBRASKA INC.	
PA	Dormady D., Stout JS., Strydom DJ., Holmquist B., Wagner FW;	
PI	DR WPI; 2000-376575/32.	
PT	Preparation of peptide with C-terminal alpha-carboxamide residue, e.g. ammonia in presence of clostripain	
PT	growth hormone releasing factors comprises treating substrate with	
PT	ammonia in presence of clostripain	
PT	Example 1; Page 16; 48pp; English.	
XX	The present sequence is a modified Glucagon Like Peptide (GLP) fragment. This sequence is composed of residues 7 to 34 of GLP, and was produced by attempted clostripain catalysed amidation of another modified GLP fragment (AAB07291) at pH 7.9. Hydrolysis at Lys34 occurred to produce the present sequence. The expected product would have had a C-terminal alpha-carboxamide residue. The peptide of AAB07291 was treated with an ammonia reagent and clostripain (also known as Clostridopeptidase B).	
CC	Clostripain is an extracellular thiol endopeptidase from Clostridia.	
CC	Clostripain cleaves arginine containing peptides amidatively at an	

RESULT 8

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

RESULT 9

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
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CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			
Db	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			

CC Arg-Xaa peptide bond.

CC Sequence 28 AA;

Query Match	100.0%	Score 144;	DB 21;	Length 28;
Best Local Similarity	100.0%	Pred. No. 2.1e-14;		
Matches	28;	Conservative	0;	Mismatches
Qy	1 HAE <del>G</del> TFTSDVSS <del>S</del> LEQQA <del>K</del> EFTAWL <del>V</del> K 28			</td

AC AAE09258;  
 DT XX  
 XX 15-NOV-2001 (first entry)  
 XX PD  
 XX XX 02-AUG-2001.  
 DE Human glucagon-like peptide-1 related molecule (GLP)-1 derivative #5.  
 XX PR  
 XX XX 16-JAN-2001; 2001WO-US00010.  
 KW Human; glucagon-like peptide-1 related molecule; GLP; GIP crystal;  
 manufacuring process; pharmaceutical formulation; therapy; diabetes;  
 obesity.  
 KW PR  
 XX OS Homo sapiens.  
 OS Synthetic.  
 XX PN US2001014666-A1.  
 XX PR 11-DEC-1998; 98US-0209799.  
 XX PD 16-AUG-2001.  
 XX PF 11-DEC-1998; 98US-0209799.  
 XX PR 11-DEC-1998; 98US-0209799.  
 XX PT (HERM/) HERMELING R N.  
 PA (HOFF/) HOFFMANN J A.  
 PA (NARA/) NARASIMHAN C.  
 XX PI Hermeling RN, Hoffmann JA, Narasimhan C;  
 DR WPI; 2001-476192/51.  
 XX PR Disclosure; Page 12; 49PP; English.  
 XX PS Glucagon-like peptide-1 crystals for treating diabetes are prepared  
 PT from mother liquor containing glucagon-like-peptide-1 related molecules  
 XX dissolved in buffered solution and alcohol.  
 XX Disclosure; Page 11; 17pp; English.  
 XX:  
 CC The present sequence is a human glucagon-like peptide-1 related molecule  
 (GLP)-1 derivative. The singl tetragonal flat rod-shaped or plate-like  
 CC crystals of a GIP are prepared from a crystallisation solution containing  
 a GIP, a buffering agent, an alcohol or a mono or disaccharide and  
 optionally ammonium sulphate or zinc. The GIP crystals are used in  
 CC manufacturing process, in pharmaceutical formulations for treating  
 CC diabetes, obesity or related conditions in mammals.  
 XX SQ Sequence 28 AA;  
 Query Match 100.0%; Score 144; DB 22; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-14;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 HAEGTFTSDVSSYLEGQAKEFIAWLK 28  
 Db 1 HAEGTFTSDVSSYLEGQAKEFIAWLK 28  
 RESULT 11  
 AAG63273  
 ID AAG63273 standard; protein; 28 AA.  
 XX AC AAG63273;  
 XX DT 01-OCT-2001 (first entry)  
 DE An insoluble glucagon-like peptide 1 (GLP-1) compound.  
 KW Glucagon-like peptide 1; GLP-1; soluble GLP-1.  
 XX OS Synthetic.  
 XX PN WO200155213-A2.  
 XX PR 16-JAN-2001; 2001WO-US00010.  
 XX PR 27-JAN-2000; 2000US-0178438.  
 XX PR 09-AUG-2000; 2000US-0224058.  
 XX PA (ELLI ) LILLY & CO ELI.  
 XX PI Prouty WFJ, Rinella JVJ;  
 XX DR WPI; 2001-476192/51.  
 XX PR  
 XX PT Preparing a Glucagon-like peptide 1 compound soluble in aqueous  
 PT solution at pH 7.4, comprises dissolving the insoluble form in aqueous  
 base or acid and neutralizing the solution -  
 PT

XX  
PS Claim 4; Page 38; 49pp; English.  
XX  
CC The present sequence represents an insoluble glucagon-like peptide 1  
CC (GLP-1). The specification describes a method for preparing a GLP-1  
CC compound that is insoluble in aqueous form at pH 7-4 from a GLP-1  
CC molecule dissolving the insoluble compound in aqueous base or acid;  
CC neutralizing the GLP-1 solution to a pH at which no amino acid  
CC racemization of the GLP-1 compound occurs; and isolating GLP-1 from  
CC the neutralized solution. The method is used to prepare a soluble form  
CC of a GLP-1 compound. The soluble form of GLP-1 is physiologically active.  
XX  
SQ Sequence 28 AA;

Query Match	Score	DB	Length	
Best Local Similarity	100.0%	2.1e-14	28	
Matches	28	0	Mismatches	0
Indels	0	Gaps	0	

Oy 1 HAEGFTSDVSSYLEGQAAKEFTAWLVK 28  
Db 1 HAEGFTSDVSSYLEGQAAKEFTAWLVK 28

RESULT 12  
ABB07145  
ID ABB07145 standard; peptide; 28 AA.  
XX  
AC ABB07145;  
XX  
DT 13-MAR-2002 (first entry)  
XX  
DE Glucagon-like peptide-1 (GLP-1) fragment (residues 7-34).  
XX  
KW - GLP-1; glucagon-like-peptide-1; growth-hormone releasing factor; GRF;  
KW parathyroid hormone; PTH; antidiabetic; anorectic; cerebroprotective;  
KW vasoconstrictor; anti-inflammatory; antiarrtherosclerotic; hepatotropic;  
KW tranquilizer; vulnerary; osteopathic; pharmaceutical.  
OS • Homo sapiens.  
XX  
PN WO200187322-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 17-MAY-2001; 2001WO-US15872.  
XX  
PR 17-MAY-2000; 2000US-20537P.  
XX  
PR 19-MAY-2000; 2000US-205262P.  
PA (BION-) BIONEBRASKA INC.  
XX  
PI Holmquist B, Dormady DC;  
XX  
DR WPI; 2002-082941/11.  
XX  
PT New peptide formulation for treating disease e.g. diabetes, obesity,  
PT ischemia comprises peptides, an acid having a specified dissociation  
PT constant and an excipient  
XX  
PS Disclosure; Page 10; 34pp; English.

The invention provides a pharmaceutical composition that comprises a  
CC molecule selected from a glucagon-like-peptide-1 (GLP-1) molecule, growth  
CC -hormone releasing factor (GRF) molecule or a parathyroid hormone (PTH)  
CC molecule. The composition further includes a weak acid such as acetic  
acid. The pH of the composition is 3 - 5. The composition can be used for  
CC the treatment of a disease or condition selected from diabetes, excess  
CC appetite, obesity, stroke, ischemia, reperfusion injury, disturbed  
CC glucose metabolism, surgery, coma, shock, gastrointestinal disease,  
CC digestive hormone disease, atherosclerotic vascular disease, gestational  
CC diabetes, liver disease and cirrhosis, glucocorticoid excess, Cushing's  
disease, the presence of activated counter regulatory hormones that occur  
CC after trauma or a disease, hypertriglyceridemia, chronic pancreatitis,  
CC the need for parenteral feeding, and a catabolic state following surgery  
or injury. The present sequence represents a GLP-1 peptide fragment.

XX  
SQ Sequence 28 AA;

Query Match	Score	DB	Length	
Best Local Similarity	100.0%	2.1e-14	28	
Matches	28	0	Mismatches	0
Indels	0	Gaps	0	

Oy 1 HAEGFTSDVSSYLEGQAAKEFTAWLVK 28  
Db 1 HAEGFTSDVSSYLEGQAAKEFTAWLVK 28

RESULT 13  
AAM0395  
ID AAM0395 standard; Peptide; 28 AA.  
XX  
AC AAM0395;  
XX  
DT 18-FEB-2002 (first entry)  
XX  
DE Glucagon-like peptide 1 (7-34).  
XX  
KW Glucagon-like peptide 1 (7-34); GLP-1 (7-34); insulinotropin;  
KW human; glycaemic; antidiabetic; insulinotrophic; NIDDM;  
KW non-insulin dependent diabetes mellitus; therapy.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN US6284727-B1.  
XX  
PD 04-SEP-2001.  
XX  
PF 07-JUN-1995; 95US-0472349.  
XX  
PR 25-JAN-1994; 94US-011655.  
PR 07-APR-1993; 93US-004133.  
XX  
PA (SCCO-) SCIOS INC.  
XX  
PI Kim Y, Lambert WJ, Qi H, Gelfand RA, Geoghegan KF, Danley DE;  
XX  
DR WPI; 2002-033119/04.  
XX  
PT Compositions useful in treatment of non-insulin dependent diabetes  
PT mellitus comprises peptides and polymer e.g. polysaccharide or  
PT vegetable oil.  
XX  
PS Claim 1(i)(c); Column 47; 42pp; English.  
XX  
CC The present sequence is that of amino acids 7-34 of glucagon-like  
CC peptide 1 (GLP-1). During processing in the pancreas and  
CC intestine, 31-amino acid GLP-1 is converted to 31-amino acid  
CC GLP-1 (7-37). This peptide has insulinotropic activity, i.e. it is  
CC able to stimulate, or cause to be stimulated, the synthesis or  
expression of insulin. GLP-1, GLP-1 (7-37) and their derivatives,  
CC including the present peptide, are used in claimed compositions for  
CC prolonged administration in the treatment of non-insulin dependent  
CC diabetes mellitus. The compositions, which also include a polymer  
CC such as a polysaccharide or vegetable oil, enhance insulin action  
CC to achieve sustained glycaemic control.  
XX  
SQ Sequence 28 AA;

Query Match	Score	DB	Length	
Best Local Similarity	100.0%	2.1e-14	28	
Matches	28	0	Mismatches	0
Indels	0	Gaps	0	

Oy 1 HAEGFTSDVSSYLEGQAAKEFTAWLVK 28

Db 1 HAEGTFTSDVSSYLEGAAKEFIAWLVK 28  
 XX  
 XX WO9325579-A.  
 PN  
 XX  
 PD 23-DEC-1993.  
 XX  
 ID AAR2424  
 XX  
 AAR24524 standard; peptide; 29 AA.  
 XX  
 AC AAR24524;  
 XX  
 DT 02-DEC-1992 (first entry).  
 XX  
 DE GLP-1 derivative.  
 XX  
 KW Maturity onset diabetes mellitus; MODM; pathogenesis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US518666-A.  
 XX  
 PD 02-JUN-1992.  
 XX  
 PR 05-MAY-1986; 86US-0859928.  
 XX  
 PR 05-MAY-1986; 86US-0859928.  
 PR 26-JAN-1988; 88US-0148517.  
 PR 01-JUN-1990; 90US-0532111.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 XX  
 PI \* Habener JF;  
 XX  
 DR WPI; 1992-208235/25.  
 XX  
 PT New glucagon-like peptide 1 derivatives - have insulinotropic activity and are used to treat Diabetes mellitus  
 PT :  
 XX  
 PS Claim 1; Page 20 and Fig 1; 16pp; English.  
 XX  
 CC The sequence given is derived from glucagon-like peptide 1 (GLP-1) and has a higher insulinotropic activity than GLP-1 (1-36) and GLP-1 (1-37). The peptide may be modified to a acid addn. or carboxylic acid addn. salt or lower alkyl ester and amide (lower (di)alkyl amide) derivative. These modified derivatives have the same insulinotropic activity as the original GLP-1 derivative. These peptides are used in the treatment of maturity onset diabetes mellitus (MODM). They may also be used in the study of MODM pathogenesis. Dosages can be administered intravenously, intramuscularly or subcutaneously.  
 XX  
 SQ Sequence 29 AA:  

Query	Match	Score	Length
Oy	1 HAEGTFTSDVSSYLEGAAKEFIAWLVK 28	100.0%	29
Db	1 HAEGTFTSDVSSYLEGAAKEFIAWLVK 28	100.0%	29

 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 Search completed: March 19, 2003, 12:10:34  
 Job time : 36 secs  
 RESULT 15  
 AAR45436  
 ID AAR45436 standard; protein; 29 AA.  
 XX  
 AC AAR45436;  
 XX  
 DT 27-JUN-1994 (first entry)  
 XX  
 DE Insulinotropin derivative.  
 XX  
 KW Insulinotropic; activity; enhancing insulin activity; treatment;  
 KW Type II diabetes.  
 XX  
 OS Synthetic.

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GenCore version 5.1.4-F5-4578

### ON protein - protein search, using sw model

Run on: March 19, 2003, 12:02:12 ; Search time 14 Seconds

(without alignments)  
58.846 Million cell updates/sec

Title: US-09-508-083-1

Perfect score: 144

Sequence: 1 HAEGTFTSDVSSYLEGQAKEFTAWLVK 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

### Database :

Issued Patents AA:\*

1: /cgn2\_6/ptodata/2/iaa5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/iaa5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/iaa6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/iaa6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/iaaPCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/2/iaa/bactfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

### ALIGNMENTS

### RESULT 1

US-09-505-162-4

; Sequence 4, Application US/08095162

GENERAL INFORMATION:

APPLICANT: Wagner, Fred W.

APPLICANT: Stout, Jay

APPLICANT: Henriksen, Dennis

APPLICANT: Partridge, Bruce

APPLICANT: Manning, Shane

TITLE OF INVENTION: Enzymatic Method for Modification of

TITLE OF INVENTION: Recombinant Polypeptides

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant & Gould

STREET: 3100 No. 5512459west Center

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPILER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08-095,162

FILING DATE: 20-JUL-1993

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Nelson, Albin J.

REGISTRATION NUMBER: 28,659

REFERENCE/DOCKET NUMBER: 8648.32-US01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-332-5300

TELEFAX: 612-332-9081

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Peptide

IMMEDIATE SOURCE:

CLONE: GFP1 (7-34)

US-08-095-162-4

Query Match 100.0%; Score 144; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 1 le-14;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 1, Appl1

Sequence 2, Appl1

Sequence 3, Appl1

Sequence 4, Appl1

Sequence 5, Appl1

Sequence 6, Appl1

Sequence 7, Appl1

Sequence 8, Appl1

Sequence 9, Appl1

Sequence 10, Appl1

RESULT 2		TITLE OF INVENTION: Enzymatic Method for Modification of Recombinant Polypeptides	
US-08-470-220A-4		SEQUENCE 4, Application US/08470220A	
Sequence 4, Application US/08967374		GENERAL INFORMATION:	
; Sequence 4, Application US/08967374		Patent No. 5707825	
; Patent No. 6037143		APPLICANT: Wagner, Fred W.	
; APPLICANT: Wagner, Fred W.		APPLICANT: Stout, Jay	
; APPLICANT: Stout, Jay		APPLICANT: Henriksen, Dennis	
; APPLICANT: Henriksen, Dennis		APPLICANT: Partidge, Bruce	
; APPLICANT: Partidge, Bruce		APPLICANT: Manning, Shane	
; APPLICANT: Manning, Shane		TITLE OF INVENTION: Enzymatic Method for Modification of Recombinant Polypeptides	
; NUMBER OF SEQUENCES: 26		TITLE OF INVENTION: Recombinant Polypeptides	
; CORRESPONDENCE ADDRESS:		CORRESPONDENCE ADDRESS:	
; ADDRESSE: Merchant & Gould		ADDRESSE: Merchant & Gould	
; STREET: 3100 No. 6037143west Center		STREET: 3100 No. 6037143west Center	
; CITY: Minneapolis		CITY: Minneapolis	
; STATE: MN		STATE: MN	
; COUNTRY: USA		COUNTRY: USA	
; ZIP: 554402		COMPUTER READABLE FORM:	
; COMPUTER: IBM PC compatible		COMPUTER: IBM PC compatible	
; OPERATING SYSTEM: PC-DOS/MS-DOS		OPERATING SYSTEM: PC-POS/MS-DOS	
; SOFTWARE: Patent Release #1.0, Version #1.30		SOFTWARE: Patent Release #1.0, Version #1.30	
; CURRENT APPLICATION DATA:		CURRENT APPLICATION DATA:	
; APPLICATION NUMBER: US/08/470,220A		APPLICATION NUMBER: US/08/957,374	
; FILING DATE: 06-JUN-1995		FILING DATE:	
; CLASSIFICATION: 435		CLASSIFICATION:	
; PRIOR APPLICATION DATA:		PRIORITY APPLICATION DATA:	
; APPLICATION NUMBER: US 08/095,162		REFERENCE DOCKET NUMBER: 8648.32-USDA-1	
; FILING DATE: 20-JUL-1993		TELECOMMUNICATION INFORMATION:	
; ATTORNEY/AGENT INFORMATION:		TELEPHONE: 612-332-5300	
; NAME: Nelson, Albin J.		TELEFAX: 612-332-9081	
; REFERENCE DOCKET NUMBER: 8648.32-US01		ATTORNEY/AGENT INFORMATION:	
; TELECOMMUNICATION INFORMATION:		NAME: Carter, Charles G.	
; TELEPHONE: 612-332-5300		REGISTRATION NUMBER: 35,093	
; TELEFAX: 612-332-9081		REFERENCE DOCKET NUMBER: 8648.32-USDA-1	
; INFORMATION FOR SEQ ID NO: 4:		TELEPHONE: 612-332-5300	
; SEQUENCE CHARACTERISTICS:		FILING DATE: 29-AUG-1995	
; LENGTH: 28		ATTORNEY/AGENT INFORMATION:	
; TYPE: amino acid		NAME: Carter, Charles G.	
; LENGTH: 28		REGISTRATION NUMBER: 35,093	
; TYPE: amino acid		REFERENCE DOCKET NUMBER: 8648.32-USDA-1	
; TOPOLOGI: linear		TELEPHONE: 612-332-5300	
; MOLECULE TYPE: Peptide		TELEFAX: 612-332-9081	
; IMMEDIATE SOURCE: peptide		INFORMATION FOR SEQ ID NO: 4:	
; CLONE: GLPI (7-34)		SEQUENCE CHARACTERISTICS:	
US-08-470-220A-4		SEQUENCE CHARACTERISTICS:	
; LENGTH: 28;		SEQUENCE CHARACTERISTICS:	
; Best Local Similarity 100.0%; Score 144; DB 1;		SEQUENCE CHARACTERISTICS:	
; Matches 28; Conservative 0; Mismatches 0;		SEQUENCE CHARACTERISTICS:	
; Indels 0; Gaps 0;		SEQUENCE CHARACTERISTICS:	
; RESULT 4		SEQUENCE CHARACTERISTICS:	
; US-08-470-349-5		SEQUENCE CHARACTERISTICS:	
; Sequence 5, Application US/08472349		SEQUENCE CHARACTERISTICS:	
; Patent No. 6284727		SEQUENCE CHARACTERISTICS:	
; GENERAL INFORMATION:		SEQUENCE CHARACTERISTICS:	
; APPLICANT: Kim, Yessoek		SEQUENCE CHARACTERISTICS:	
; APPLICANT: Lambert, William J.		SEQUENCE CHARACTERISTICS:	
; APPLICANT: Oi, Hong		SEQUENCE CHARACTERISTICS:	
; APPLICANT: Gelfand, Robert A.		SEQUENCE CHARACTERISTICS:	
; APPLICANT: Geoghegan, Kieran F.		SEQUENCE CHARACTERISTICS:	
; APPLICANT: Danley, Dennis E.		SEQUENCE CHARACTERISTICS:	
; TITLE OF INVENTION: Prolonged Delivery of Peptides		SEQUENCE CHARACTERISTICS:	
; NUMBER OF SEQUENCES: 7		SEQUENCE CHARACTERISTICS:	
; CORRESPONDENCE ADDRESS:		CORRESPONDENCE ADDRESS:	
; ADDRESSE: Pfizer Inc		ADDRESSE: Pfizer Inc	
; STREET: 235 East 42nd Street, 20th Floor		STREET: 235 East 42nd Street, 20th Floor	
; CITY: New York		CITY: New York	
; STATE: New York		STATE: New York	
; COUNTRY: U.S.A.		COUNTRY: U.S.A.	
; ZIP: 10017-5755		COMPUTER READABLE FORM:	
; COMPUTER: IBM PC compatible		COMPUTER: IBM PC compatible	
; OPERATING SYSTEM: PC-DOS/MS-DOS		OPERATING SYSTEM: PC-DOS/MS-DOS	
; SOFTWARE: Patent Release #1.0, Version #1.25		SOFTWARE: Patent Release #1.0, Version #1.25	

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,349  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/08/181,655  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sheyka, Robert F.  
 REGISTRATION NUMBER: 31,304  
 REFERENCE/DOCKET NUMBER: PCB391  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)573-1189  
 TELEX: (212)573-1939  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 28 amino acids  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE:  
 ORGANISM: N/A  
 STRAIN: N/A  
 INDIVIDUAL ISOLATE: N/A  
 HAPLOTYPE: N/A  
 CELL LINE: N/A  
 IMMEDIATE SOURCE:  
 LIBRARY: N/A  
 CLONE: N/A  
 POSITION IN GENOME:  
 CHROMOSOME SEGMENT: N/A  
 MAP POSITION: N/A  
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 09-209-799D-8  
 Query Match 100.0%; Score 144; DB 4; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-14; Indels 0; Gaps 0;  
 Matches 28; Conservative 0; Mismatches 0;  
 CURRENT PILING DATE: 1998-12-11  
 NUMBER OF SEQ ID NOS: 29  
 SOFTWARE: PatentIn version 3.0  
 EQ ID NO 8  
 LENGTH: 28  
 TYPE: PRT  
 ORGANISM: Artificial  
 FEATURE:  
 OTHER INFORMATION: synthetic construct  
 09-209-799D-8

RESULT 6  
 US-09-505-991-4  
 Sequence 4, Application US/09505991  
 ; Patent No. 6403361  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wagner, Fred W.  
 ; STOUT, Jay  
 ; Henriksen, Dennis  
 ; Partidge, Bruce  
 ; Manning, Shane  
 TITLE OF INVENTION: Enzymatic Method for Modification of Recombinant Polypeptides  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merchant & Gould  
 STREET: 3100 No. 6403361west Center  
 CITY: Minneapolis  
 STATE: MN  
 COUNTRY: USA  
 ZIP: 55402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.3.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/505,991  
 FILING DATE: 17-Feb-2000  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 PRIORITY NUMBER: 08/520,485  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Carter, Charles G.  
 REGISTRATION NUMBER: 35,093  
 REFERENCE/DOCKET NUMBER: 8648.32-USDI  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 612-332-5300  
 TELEX: 612-332-9081  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 28 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 CLONE: GPL (7-34)  
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 US-09-505-991-4  
 Query Match 100.0%; Score 144; DB 4; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-14; Indels 0; Gaps 0;  
 Matches 28; Conservative 0; Mismatches 0;  
 CURRENT PILING DATE: 1998-12-11  
 NUMBER OF SEQ ID NOS: 29  
 SOFTWARE: PatentIn version 3.0  
 EQ ID NO 8  
 LENGTH: 28  
 TYPE: PRT  
 ORGANISM: Artificial  
 FEATURE:  
 OTHER INFORMATION: synthetic construct  
 09-212-663-5  
 Sequence 5, Application US/09212663  
 ; Patent No. 6461834  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DORMADY, Dan  
 ; APPLICANT: STOUT, Jay S.  
 ; APPLICANT: STRYDOM, Daniel J

QY  
 Db  
 1 HAEGTFISDVSSYLEGQAEEKFLAWLK 28

APPLICANT: HOLMQUIST, Barton  
 ALIMENT: WAGNER, Fred W.  
 TITLE OF INVENTION: ENZYMATIC AMIDATION OF PEPTIDES  
 FILE REFERENCE: 08187/0162  
 CURRENT APPLICATION NUMBER: US/09/212,663  
 PRIORITY FILING DATE: 1998-12-16  
 PRIOR FILING DATE: 1998-11-06  
 NUMBER OF SEQ ID NOS: 25  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 5  
 LENGTH: 28  
 TYPE: PRT  
 ORGANISM: Escherichia coli  
 US-09-212-663-5

RESULT 8  
 PCT-US95-15800-21  
 Sequence 21, Application PC/TUS9515800  
 GENERAL INFORMATION:  
 APPLICANT: BioNebraska, Inc.  
 TITLE OF INVENTION: PRODUCTION OF PEPTIDES USING RECOMBINANT FUSION PROTEIN CONSTRICTS  
 NUMBER OF SEQUENCES: 33  
 ADDRESS: Merchant & Gould  
 STREET: 3100 Northwest Center, 90 S. 7th Street  
 CITY: Minneapolis  
 STATE: MN  
 COUNTRY: U.S.A.  
 ZIP: 55402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/15800  
 FILING DATE: 07-DEC-1995  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/350,530  
 FILING DATE: 07-DEC-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Carter, Charles G.  
 REGISTRATION NUMBER: 35,093  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 612/332-5300  
 TELEFAX: 612/332-9081  
 TELEX: 612/332-9081  
 INFORMATION FOR SEQ ID NO: 21:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 28 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-095-162-18

Query Match 100.0%; Score 144; DB 5; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-14; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAGCTFTSDVSSYLEGQAKEFTAWLVK 28  
 Db 1 HAGCTFTSDVSSYLEGQAKEFTAWLVK 28

RESULT 9  
 US-08-095-162-18  
 Sequence 18, Application US/08095162  
 GENERAL INFORMATION:  
 PATENT NO. 5512459  
 APPLICANT: Wagner, Fred W.  
 APPLICANT: Stout, Jay  
 APPLICANT: Henriksen, Dennis  
 APPLICANT: Partridge, Bruce  
 APPLICANT: Manning, Shane  
 TITLE OF INVENTION: Enzymatic Method for Modification of Recombinant Polypeptides  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merchant & Gould  
 STREET: 3100 No. 5512459west. Center  
 CITY: Minneapolis  
 STATE: MN  
 COUNTRY: USA  
 ZIP: 55402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/095,162  
 FILING DATE: 20-JUL-1993  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nelson, Albin J.  
 REGISTRATION NUMBER: 28,659  
 REFERENCE/DOCKET NUMBER: 8648.32-US01  
 INFORMATION FOR SEQ ID NO: 18:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 29 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-095-162-18

Query Match 100.0%; Score 144; DB 1; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-14; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 HAGCTFTSDVSSYLEGQAKEFTAWLVK 28

RESULT 10  
 US-08-470-220A-18  
 Sequence 18, Application US/08470220A  
 PATENT NO. 5707826  
 GENERAL INFORMATION:  
 APPLICANT: Wagner, Fred W.  
 APPLICANT: Stout, Jay  
 APPLICANT: Henriksen, Dennis  
 APPLICANT: Partridge, Bruce  
 APPLICANT: Manning, Shane  
 TITLE OF INVENTION: Enzymatic Method for Modification of

US-09-508-083-1.ra1

TITLE OF INVENTION: Recombinant Polypeptides  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merchant & Gould  
 STREET: 3100 No. 5707826west Center  
 CITY: Minneapolis  
 STATE: MN  
 COUNTRY: USA  
 ZIP: 55402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/470,220A  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/095,162  
 FILING DATE: 20-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nelson, Albin J.  
 REGISTRATION NUMBER: 28,659  
 REFERENCE/DOCKET NUMBER: 8648.32-US01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 612-332-5300  
 TELEX: 612-332-9081  
 INFORMATION FOR SEQ ID NO: 18:  
 SEQENCE CHARACTERISTICS:  
 LENGTH: 29 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US-08-470-220A-18

Query Match 100.0%; Score 144; DB 1; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-14;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HAEGTFTSDVSSYLEGQAKEFIawlVK 28  
 Db 1 HAEGTFTSDVSSYLEGQAKEFIawlVK 28

RESULT 11  
 US-08-967-374-18  
 ; Sequence 18, Application US/0896774  
 ; Patent No. 6037143  
 GENERAL INFORMATION:  
 APPLICANT: Wagner, Fred W.  
 APPLICANT: Stoltz, Jay  
 APPLICANT: Henriksen, Dennis  
 APPLICANT: Parridge, Bruce  
 APPLICANT: Manning, Shane  
 TITLE OF INVENTION: Enzymatic Method for Modification of  
 TITLE OF INVENTION: Recombinant Polypeptides  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merchant & Gould  
 STREET: 3100 No. 6037143west Center  
 CITY: Minneapolis  
 STATE: MN  
 COUNTRY: USA  
 ZIP: 55402  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/181,655  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/472,349  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Shieyka, Robert F.  
 REGISTRATION NUMBER: 31,304  
 REFERENCE/DOCKET NUMBER: PC8391  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)573-1189  
 TELEX: N/A  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQENCE CHARACTERISTICS:  
 LENGTH: 29 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/520,485  
 FILING DATE: 29-AUG-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Carter, Charles G.  
 REGISTRATION NUMBER: 35,093  
 REFERENCE/DOCKET NUMBER: 8648.32-US01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 612-332-5300  
 TELEX: 612-332-9081  
 INFORMATION FOR SEQ ID NO: 18:  
 SEQENCE CHARACTERISTICS:  
 LENGTH: 29 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-967-374-18

Query Match 100.0%; Score 144; DB 3; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-14;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HAEGTFTSDVSSYLEGQAKEFIawlVK 28  
 Db 1 HAEGTFTSDVSSYLEGQAKEFIawlVK 28

RESULT 12  
 US-08-472-349-4  
 Sequence 4, Application US/08472349  
 PATENT NO. 6284727  
 GENERAL INFORMATION:  
 APPLICANT: Kim, Yesook  
 APPLICANT: Lambert, William J.  
 APPLICANT: Qi, Hong  
 APPLICANT: Gelbard, Robert A.  
 APPLICANT: Geoghegan, Kieran F.  
 APPLICANT: Danley, Dennis E.  
 TITLE OF INVENTION: Prolonged Delivery of Peptides  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pfizer Inc  
 STREET: 235 East 42nd Street, 20th Floor  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10017-5755  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/472,349  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/181,655  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Shieyka, Robert F.  
 REGISTRATION NUMBER: 31,304  
 REFERENCE/DOCKET NUMBER: PC8391  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)573-1189  
 TELEX: N/A  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQENCE CHARACTERISTICS:  
 LENGTH: 29 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single

TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE:  
 ORGANISM: N/A  
 STRAIN: N/A  
 INDIVIDUAL ISOLATE: N/A  
 HAPLOTYPE: N/A  
 CELL LINE: N/A  
 IMMEDIATE SOURCE:  
 LIBRARY: N/A  
 CLONE: N/A  
 POSITION IN GENOME:  
 CHROMOSOME SEGMENT: N/A  
 MAP POSITION: N/A  
 US-08-472-345-4

Query Match 100.0%; Score 144; DB 4; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-14; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13  
 US-09-209-799D-9

Sequence 9, Application US/09209799D  
 GENERAL INFORMATION:  
 APPLICANT: Hermeling, Ronald  
 APPLICANT: Narasimhan, Chakravarthy  
 TITLE OF INVENTION: GLUCAGON-LIKE PEPTIDE-1 CRYSTALS  
 CURRENT APPLICATION NUMBER: US/09/209,799D  
 CURRENT FILING DATE: 1998-12-11  
 NUMBER OF SEQ ID NOS: 29  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 9  
 LENGTH: 29  
 TYPE: PRP  
 ORGANISM: Artificial  
 OTHER INFORMATION: synthetic construct  
 US-09-209-799D-9

Query Match 100.0%; Score 144; DB 4; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-14; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAEGTFTSDVSSYLEGQAKEFIAWLVK 28  
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RESULT 14  
 US-09-505-991-18

Sequence 18, Application US/09505991  
 Patent No. 6403361  
 GENERAL INFORMATION:  
 APPLICANT: Wagner, Fred W.  
 Scout, Jay  
 Henriksen, Dennis  
 Partridge, Bruce  
 Manning, Shane  
 TITLE OF INVENTION: Recombinant Method for Modification of  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:

RESULT 15  
 US-08-066-480-6

Sequence 6, Application US/08066480  
 Patent No. 5424286  
 GENERAL INFORMATION:  
 APPLICANT: Eng, John  
 TITLE OF INVENTION: Pharmaceutical Compositions And Use of  
 TITLE OF INVENTION: Exendin-3 and Exendin-4 for Treatment of Diabetes Mellitus  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Allegretti & Witcoff, Ltd.  
 STREET: 10 S. Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/066,480  
 FILING DATE: 24-MAR-1993  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McDonnell, John J  
 REGISTRATION NUMBER: 26,949  
 REFERENCE/DOCKET NUMBER: 93,084  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..30  
OTHER INFORMATION: /label="GLP-1-7-35  
; OTHER INFORMATION: /note="GLP-1(7-36) fragment"  
US-08-066-480-6

Query Match 100 %; Score 144; DB 1; Length 30;  
Best Local Similarity 100 %; Pred. No. 1.2e-14;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HAEGRFTSDVSSYLEGQAAKEFTIAWLVK 28  
Db 1 HAEGRFTSDVSSYLEGQAAKEFTIAWLVK 28

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GenCore version 5.1.4-P5\_4578

OM protein - protein search, using sw model

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106.924 Million cell updates/sec

Title: US-09-508-083-1

Perfect score: 144

Sequence: 1 HAGTFTSDVSSYLEQAAKEFIAWLVK 28

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Maximum DB seq length: 0

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Maximum Match 0%

Post-processing: Minimum Match 0%

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Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	144	100.0	29	9 US-09-834-229A-3
3	144	100.0	29	9 US-09-937-792-9
4	144	100.0	30	9 US-10-12-251-251
5	144	100.0	30	9 US-09-834-229A-5
6	144	100.0	30	9 US-09-937-792-5
7	144	100.0	30	10 US-09-851-738-4
8	144	100.0	30	10 US-09-805-507-4
9	144	100.0	30	10 US-09-859-804-4
10	144	100.0	30	10 US-09-859-804-4
11	144	100.0	30	10 US-09-937-792-4
12	144	100.0	30	12 US-10-072-540A-4
13	144	100.0	31	9 US-09-834-229A-1
14	100.0	31	9 US-09-937-792-1	
15	144	100.0	31	9 US-10-033-950-19
16	144	100.0	31	10 US-09-754-723-1
17	144	100.0	31	10 US-09-420-785A-3
18	144	100.0	31	10 US-09-876-388-2
19	100.0	31	10 US-09-876-388-17	

### ALIGNMENTS

RESULT 1

Best Local Similarity 100.0%; Pred. No. 2 7e-15; Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 HAGTFTSDVSSYLEQAAKEFIAWLVK 28

Db 1 HAGTFTSDVSSYLEQAAKEFIAWLVK 28

GENERAL INFORMATION:

APPLICANT: Efendic, Suad

SEQUENCE OF INVENTION: USE OF GLP-1 OR ANALOGS IN TREATMENT OF MYOCARDIAL INFARCTION

FILE REFERENCE: X-10822A

CURRENT APPLICATION NUMBER: US/09/834, 229A

CURRENT FILING DATE: 2001-04-12

PRIOR APPLICATION NUMBER: US 08/915, 918

PRIOR FILING DATE: 1997-08-21  
 PRIORITY APPLICATION NUMBER: US 06/024, 980  
 PRIOR FILING DATE: 1996-08-30  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 3  
 LENGTH: 29  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: synthetic construct  
 NAME/KEY: MISC\_FEATURE  
 LOCATION: (29)..(29)  
 OTHER INFORMATION: Xaa at position 29 is absent or Gly.  
 US-09-834-229A-3

Query Match 100.0%; Score 144; DB 9; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-15; Mismatches 0; Indels 0; Gaps 0;  
 Matches 28; Conservative 0; MisMatches 0;

QY 1 HAEGTFTSDVSSYLEGQAKEFTAWLVK 28  
 Db 1 HAEGTFTSDVSSYLEGQAKEFTAWLVK 28

RESULT 3  
 US-09-997-792-9  
 ; Sequence 9, Application US/09997792  
 ; Publication No. US20030045464A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Hermeling, Ronald  
 ; APPLICANT: Hoffmann, James  
 ; APPLICANT: Narasimhan, Chakravarthy  
 ; TITLE OF INVENTION: GLUCAGON-LIKE PEPTIDE-1 CRYSTALS  
 ; FILE REFERENCE: X-10242  
 ; CURRENT APPLICATION NUMBER: US/09/997,792  
 ; CURRENT FILING DATE: 2001-11-30  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 9  
 ; LENGTH: 29  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthetic construct  
 US-09-997-792-9

Query Match 100.0%; Score 144; DB 9; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-15; Mismatches 0; Indels 0; Gaps 0;  
 Matches 28; Conservative 0; MisMatches 0;

QY 1 HAEGTFTSDVSSYLEGQAKEFTAWLVK 28  
 Db 1 HAEGTFTSDVSSYLEGQAKEFTAWLVK 28

RESULT 4  
 US-10-125-255-1  
 ; Sequence 1, Application US/10125255  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gallaway, John A  
 ; APPLICANT: Hoffman, James A  
 ; TITLE OF INVENTION: Glucagon-Like Insulnotropic Peptides, Compositions and Methods  
 ; FILE REFERENCE: X-332E  
 ; CURRENT APPLICATION NUMBER: US/10/125,255  
 ; CURRENT FILING DATE: 2002-04-17  
 ; PRIOR APPLICATION NUMBER: 09/5573,809  
 ; PRIOR FILING DATE: 2000-05-18  
 ; NUMBER OF SEQ ID NOS: 1  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 30  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthetic construct  
 US-09-997-792-10

Query Match 100.0%; Score 144; DB 9; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-15; Mismatches 0; Indels 0; Gaps 0;  
 Matches 28; Conservative 0; MisMatches 0;

QY 1 HAEGTFTSDVSSYLEGQAKEFTAWLVK 28  
 Db 1 HAEGTFTSDVSSYLEGQAKEFTAWLVK 28

RESULT 5  
 US-09-834-229A-5  
 ; Sequence 5, Application US/09934229A  
 ; Publication No. US20030022823A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Efendic, Suad  
 ; TITLE OF INVENTION: USE OF GLP-1 OR ANALOGS IN TREATMENT OF MYOCARDIAL INFARCTION  
 ; FILE REFERENCE: X-1082A  
 ; CURRENT APPLICATION NUMBER: US/09/834, 229A  
 ; CURRENT FILING DATE: 2001-04-12  
 ; PRIOR APPLICATION NUMBER: US 08/915, 918  
 ; PRIOR FILING DATE: 1997-08-21  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 5  
 ; LENGTH: 30  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthetic construct  
 US-09-834-229A-5

Query Match 100.0%; Score 144; DB 9; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-15; Mismatches 0; Indels 0; Gaps 0;  
 Matches 28; Conservative 0; MisMatches 0;

QY 1 HAEGTFTSDVSSYLEGQAKEFTAWLVK 28  
 Db 1 HAEGTFTSDVSSYLEGQAKEFTAWLVK 28

RESULT 6  
 US-09-997-792-10  
 ; Sequence 10, Application US/09997792  
 ; Publication No. US20030045464A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hermeling, Ronald  
 ; APPLICANT: Hoffmann, James  
 ; APPLICANT: Narasimhan, Chakravarthy  
 ; TITLE OF INVENTION: GLUCAGON-LIKE PEPTIDE-1 CRYSTALS  
 ; FILE REFERENCE: X-10242  
 ; CURRENT APPLICATION NUMBER: US/09/997,792  
 ; CURRENT FILING DATE: 2001-11-30  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 10  
 ; LENGTH: 30  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthetic construct  
 US-09-997-792-10

Query Match 100.0%; Score 144; DB 9; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-15;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAE~~GTF~~SDVSSYLEGQA~~K~~EFTAWL~~V~~K 28  
 DB 1 HAE~~GTF~~SDVSSYLEGQA~~K~~EFTAWL~~V~~K 28

RESULT 7  
 US-09-851-738-4  
 ; Sequence 4, Application US/09851738  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COOLIDGE, Thomas R.  
 ; TITLE OF INVENTION: Metabolic Intervention with GLP-1 to Improve the Function of FILE REFERENCE: P03660US1  
 CURRENT APPLICATION NUMBER: US/09/851,738  
 PRIORITY FILING DATE: 2001-03-09  
 PRIORITY APPLICATION NUMBER: 09/302,596  
 PRIOR FILING DATE: 1999-04-30  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 4  
 LENGTH: 30  
 TYPE: PRT  
 ORGANISM: mammalian  
 US-09-851-738-4

Query Match 100.0%; Score 144; DB 10; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-15;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAE~~GTF~~SDVSSYLEGQA~~K~~EFTAWL~~V~~K 28  
 DB 1 HAE~~GTF~~SDVSSYLEGQA~~K~~EFTAWL~~V~~K 28

RESULT 8  
 US-09-805-507-4  
 ; Sequence 4, Application US/09805507  
 ; Patent No. US2002008195A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COOLIDGE, THOMAS R.  
 ; TITLE OF INVENTION: TREATMENT OF ACUTE CORONARY SYNDROME WITH GLP-1 FILE REFERENCE: 083187-0395  
 CURRENT APPLICATION NUMBER: US/09/805,507  
 CURRENT FILING DATE: 2001-03-14  
 PRIORITY FILING DATE: 2001-05-13  
 PRIORITY APPLICATION NUMBER: 09/859,804  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 4  
 LENGTH: 30  
 TYPE: PRT  
 ORGANISM: Unknown Organism  
 FEATURE:  
 ; OTHER INFORMATION: Description of Unknown Organism: Mammalian GLP  
 ; OTHER INFORMATION: peptide  
 US-09-805-507-4

Query Match 100.0%; Score 144; DB 10; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-15;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAE~~GTF~~SDVSSYLEGQA~~K~~EFTAWL~~V~~K 28  
 DB 1 HAE~~GTF~~SDVSSYLEGQA~~K~~EFTAWL~~V~~K 28

RESULT 9  
 US-09-859-804-4  
 ; Sequence 4, Application US/09859804  
 ; Patent No. US20020107206A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COOLIDGE, THOMAS R.  
 ; TITLE OF INVENTION: TREATMENT OF ACUTE CORONARY SYNDROME WITH GLP-1 FILE REFERENCE: 083187-0395  
 CURRENT APPLICATION NUMBER: US/09/859,804  
 CURRENT FILING DATE: 2001-03-18  
 PRIORITY FILING DATE: 2000-05-19  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 4  
 LENGTH: 30  
 TYPE: PRT  
 ORGANISM: Unknown Organism  
 FEATURE:  
 ; OTHER INFORMATION: Description of Unknown Organism: Mammalian GLP  
 ; OTHER INFORMATION: peptide  
 US-09-859-804-4

Query Match 100.0%; Score 144; DB 10; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-15;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAE~~GTF~~SDVSSYLEGQA~~K~~EFTAWL~~V~~K 28  
 DB 1 HAE~~GTF~~SDVSSYLEGQA~~K~~EFTAWL~~V~~K 28

RESULT 10  
 US-09-942-978-4  
 ; Sequence 4, Application US/09982978  
 ; Patent No. US20020146405A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: COOLIDGE, THOMAS R.  
 ; TITLE OF INVENTION: TREATMENT OF ACUTE CORONARY SYNDROME WITH GLP-1 FILE REFERENCE: 083187-0395  
 CURRENT APPLICATION NUMBER: US/09/982,978  
 CURRENT FILING DATE: 2001-10-22  
 PRIORITY FILING DATE: 2001-05-18  
 PRIORITY APPLICATION NUMBER: 09/859,804  
 PRIORITY FILING DATE: 2000-05-19  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 4  
 LENGTH: 30  
 TYPE: PRT  
 ORGANISM: Unknown Organism  
 FEATURE:  
 ; OTHER INFORMATION: Description of Unknown Organism: Mammalian GLP  
 ; OTHER INFORMATION: peptide  
 US-09-942-978-4

Query Match 100.0%; Score 144; DB 10; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-15;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HAE~~GTF~~SDVSSYLEGQA~~K~~EFTAWL~~V~~K 28  
 DB 1 HAE~~GTF~~SDVSSYLEGQA~~K~~EFTAWL~~V~~K 28

RESULT 11  
 US-09-933-021B-4  
 ; Sequence 4, Application US/09953021B  
 ; Patent No. US2002014713A1  
 ; GENERAL INFORMATION:

APPLICANT: Coolidge, Thomas L.  
 TITLE OF INVENTION: Metabolic Intervention with GTP to Improve the Function of Ischemic Tissue  
 FILE REFERENCE: P0360US6  
 CURRENT APPLICATION NUMBER: US/09/953, 021B  
 CURRENT FILING DATE: 2001-09-11  
 PRIOR APPLICATION NUMBER: 09/302, 596  
 PRIOR FILING DATE: 1999-04-30  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 4  
 LENGTH: 30  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-953-021B-4

Query Match 100.0%; Score 144; DB 10; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-15;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12  
 US-10-072-540A-4  
 ; Sequence 4, Application US/10072540A  
 ; Patent No. US20030123466A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hoffmann, James  
 ; TITLE OF INVENTION: GLP-1 FORMULATIONS  
 ; FILE REFERENCE: X-11368A  
 ; CURRENT APPLICATION NUMBER: US/10/072, 540A  
 ; CURRENT FILING DATE: 2002-02-08  
 ; PRIOR APPLICATION NUMBER: US 60/067, 600  
 ; PRIOR FILING DATE: 1997-12-05  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4  
 LENGTH: 30  
 TYPE: PRT  
 NAME/KEY: MOD\_RES  
 FEATURE: Homo sapiens  
 LOCATION: (30)..(30)  
 OTHER INFORMATION: AMIDATION  
 US-10-072-540A-4

Query Match 100.0%; Score 144; DB 12; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-15;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13  
 US-09-834-229A-1  
 ; Sequence 1, Application US/09834229A  
 ; Publication No. US20030022823A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Eberle, Sعاد  
 ; TITLE OF INVENTION: USE OF GLP-1 OR ANALOGS IN TREATMENT OF MYOCARDIAL INFARCTION  
 ; FILE REFERENCE: X-10822A  
 ; CURRENT APPLICATION NUMBER: US/09/834, 229A  
 ; CURRENT FILING DATE: 2001-04-12  
 ; PRIOR APPLICATION NUMBER: US 08/915, 918  
 ; PRIOR FILING DATE: 1997-08-21  
 ; PRIOR APPLICATION NUMBER: US 06/024, 980  
 ; PRIOR FILING DATE: 1996-08-30  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: PatentIn Version 3.0  
 ; SEQ ID NO 19  
 LENGTH: 31  
 TYPE: PRT  
 ORGANISM: artificial sequence  
 OTHER INFORMATION: glucagon-like peptide 1  
 US-10-093-958-19

Query Match 100.0%; Score 144; DB 9; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 3e-15;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14  
 US-09-997-792-1  
 ; Sequence 1, Application US/09997792  
 ; Publication No. US20030045464A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hermeling, Ronald  
 ; APPLICANT: Hoffmann, James  
 ; APPLICANT: Narasimhan, Chakravarthy  
 ; TITLE OF INVENTION: GLUCAGON-LIKE PEPTIDE-1 CRYSTALS  
 ; FILE REFERENCE: X-10424  
 ; CURRENT APPLICATION NUMBER: US/09/997, 792  
 ; CURRENT FILING DATE: 2001-11-30  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SEQ ID NO 1  
 LENGTH: 31  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-997-792-1

Query Match 100.0%; Score 144; DB 9; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 3e-15;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15  
 US-10-093-958-19  
 ; Sequence 19, Application US/10093958  
 ; Publication No. US2003004423A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gillies, Stephen  
 ; APPLICANT: Jeffrey, Way  
 ; TITLE OF INVENTION: Expression Technology for Proteins Containing a Hybrid Iso-type  
 ; TITLE OF INVENTION: Molety  
 ; FILE REFERENCE: LEX-016  
 ; CURRENT APPLICATION NUMBER: US/10/093, 958  
 ; CURRENT FILING DATE: 2002-03-07  
 ; PRIOR APPLICATION NUMBER: US 60/274, 096  
 ; PRIOR FILING DATE: 2001-03-07  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: PatentIn Version 3.0  
 ; SEQ ID NO 19  
 LENGTH: 31  
 TYPE: PRT  
 ORGANISM: artificial sequence  
 OTHER INFORMATION: glucagon-like peptide 1  
 US-10-093-958-19

Wed Mar 19 12:17:53 2003

us-09-508-083-1.rapb

Oy	1	HAEGTTSDVSSYLEQQAKEFIawlVK	28
	1		
Db	1	HAEGTTSVDSSYLEQQAKEFIawlVK	28

Search completed: March 19, 2003, 12:09:50  
Job time : 15 secs

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OM protein - protein search, using sw model

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GenCore version 5.1.4\_P5 4578

Title: US-09-508-083-1

Perfect score: 144

Sequence: 1 HABGTFTSDVSVLEGGAAKEFTAWLVK 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result NO.	Score	Query Match Length	DB ID	Description
1	144	100.0	158	GCPG glucagon precursor - pig (fragment)
2	144	100.0	180	1 GCHU glucagon precursor
3	144	100.0	180	1 GCGP glucagon precursor
4	144	100.0	180	1 GCRDU glucagon precursor
5	144	100.0	180	1 GCRT glucagon precursor
6	144	100.0	180	1 GCHO glucagon precursor
7	144	100.0	180	1 GCPB glucagon precursor
8	144	100.0	180	2 A57294 glucagon precursor
9	132	91.7	151	1 GCH glucagon precursor
10	132	91.7	206	2 I01301 glucagon precursor - chick
11	118	81.9	30	2 B61125 glucagon-like pept
12	118	81.9	30	2 C61125 glucagon-like pept
13	118	81.9	101	1 GCIGB glucagon precursor
14	112	77.8	63	1 GCIDC glucagon precursor
15	112	77.8	122	1 GCAF2 glucagon precursor
16	110	76.4	72	1 GCGKA glucagon precursor
17	109	75.7	66	2 I51093 glucagon - chinook
18	109	75.7	178	2 I51057 glucagon I precur
19	109	75.7	178	2 I51057 glucagon II precur
20	104	72.2	30	2 S44473 glucagon precursor
21	104	72.2	60	1 GCONC glucagon precursor
22	97	67.4	29	2 S07211 glucagon - marbled
23	97	67.4	87	1 GCFIS glucagon precursor
24	95	66.0	29	1 GCDP glucagon - smaller
25	93	64.6	29	1 GCEN glucagon - elephant
26	93	64.6	124	1 GCAF glucagon 1 precurs
27	90	62.5	1 GCGO glucagon - North A	
28	90	62.5	29	2 A91741 glucagon - turkey
29	2			

**ALIGNMENTS**

RESULT 1

GCPG glucagon precursor - pig (fragment)

N;Alternate names: glicentin; oxyntomodulin

N;Contains: glicentin-related peptide; glucagon; glucagon-37 (oxyntomodulin); glucago

C;Species: Sus scrofa domesticus (domestic pig)

C;Date: 17-Dec-1982 #sequence\_revision 31-Mar-1993 #text\_change 20-Mar-1998

C;Accession: A01540; A60312; A91781; B32614; A28064

R;Thim, L.; Moody, A.J.

Regul. Pept. 2, 139-150, 1981

A;Title: The primary structure of porcine glicentin (proglucagon).

A;Reference number: A94233; MUID:81248172; PMID:6894800

A;Accession: A01540

A;Molecule type: protein

A;Residues: 1-69 <THI>

R;Thim, L.; Moody, A.J.

Regul. Pept. Suppl. 2, S33, 1983

A;Title: Primary structure of a possible porcine proglucagon fragment.

A;Reference number: A60312

A;Accession: A60312

A;Molecule type: protein

A;Residues: 1-30 <THI>

A;Note: this peptide is co-secreted with glucagon from the pancreas

R;Bromer, W.W.; Sinn, L.G.; Behrens, O.K.

J Am Chem Soc 79, 2807-2810, 1957

A;Title: The amino acid sequence of glucagon. V. Location of amide groups, acid degra

A;Reference number: A91781

A;Accession: A91781

A;Molecule type: protein

A;Residues: 33-61 <BRO>

R;Orskov, C.; Bersani, M.; Johansen, A.H.; Hojrup, P.; Holst, J.J.

J Biol. Chem. 264, 12826-12829, 1989

A;Title: Complete sequences of glucagon-like peptide-1 from human and pig small intes

A;Reference number: A92732; MUID:89327238; PMID:2753890

A;Accession: B32614

A;Molecule type: protein

A;Residues: 78-107 <ORS>

R;Buhl, T.; Thim, L.; Kofod, H.; Orskov, C.; Harling, H.; Holst, J.J.

J. Biol. Chem. 263, 8621-8624, 1988

A;Title: Naturally occurring products of proglucagon 111-160 in the porcine and human

A;Reference number: A28064; MUID:88243712; PMID:3379036

A;Accession: A28064

A;Molecule type: protein

A;Residues: 111-15 <BUH>

C;Comment: X's represent missing amino acids, mostly basic, that are predicted to ext

C;Superfamily: glucagon

C;Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; int

F;1-69/Product: glucagon-69 #status experimental <669>

F;1-30/Product: glicentin-related peptide #status experimental

F;33-69/Product: glucagon-37 #status predicted <G37>

F;33-61/Product: glucagon-37 #status experimental <GCN>

F;78-107/Product: glucagon-like peptide 1 #status experimental <GLI>

F;126-158/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gln	Oy	1	HAEGETTSVDVSYLEGGAAKEFTIWLWIK	28	GCHU
Query Match 100.0%; Score 144; DB 1; Length 158;					
Best Local Similarity 100.0%; Pred. No. 1.1e-13; Mismatches 0;					
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
<b>RESULT 2</b>					
glucagon precursor [validated] - human					
N;Contains: glicentin; glicentin-related polypeptide (GRPP); glucagon; glucagon-like peptide 1 (GICP1)					
C;Species: Homo sapiens (man)					
C;Date: 24-Apr-1984 #sequence_revision 31-Mar-1993 #text_change 08-Dec-2000					
C;Accession: A24377; R44197; A30875; A32614; A01541; S23509					
R;White, J.W.; Saunders, G.F.					
Nucleic Acids Res. 14: 4719-4730, 1986					
A;Title: Structure of the human glucagon gene.					
A;Reference number: A24377; MUID:86259053; PMID:3125587					
A;Accession: A24377					
A;Molecule type: DNA					
A;Residues: 1-180 <WH1>					
A;Cross-references: GB:X03991					
R;Bell, G.I.; Sanchez-Pescador, R.; Laybourn, P.J.; Nadrian, R.C.					
Nature 244, 368-371, 1983					
A;Title: Exon duplication and divergence in the human preproglucagon gene.					
A;Reference number: A44197; MUID:83271477; PMID:6877358					
A;Accession: A44197					
A;Residues: 1-179 <BEL2>					
A;Cross-references: GB:V01515; NID:931777; PIDN:CAA24759.1; PID:931778					
A;Molecule type: DNA					
A;Accession: A30875					
R;Drucker, D.J.; Asa, S.					
J. Biol. Chem. 263, 13475-13478, 1988					
A;Title: Glucagon gene expression in vertebrate brain					
A;Reference number: A30875; MUID:88330860; PMID:2901414					
A;Accession: A30875					
A;Molecule type: mRNA					
A;Residues: 1-180 <DRD>					
A;Cross-references: GB:J04040; NID:182029; PIDN:BAA2567.1; PID:183270					
R;Orskov, C.; Bersani, M.; Johansen, A.H.; Hojrup, P.; Holst, J.J.					
J. Biol. Chem. 264, 12826-12829, 1989					
A;Title: Complete sequences of glucagon-like peptide-1 from human and pig small intestine					
A;Reference number: A92732; MUID:89327238; PMID:253890					
A;Accession: A32614					
A;Molecule type: protein					
A;Residues: 98-127 <CRS>					
R;Thomsen, J.; Kristiansen, K.; Brunfeldt, K.; Sundby, F.					
FEBs Lett. 21, 315-319, 1972					
A;Title: The amino acid sequence of human glucagon.					
A;Reference number: A91373					
A;Accession: A01541					
A;Molecule type: protein					
A;Residues: 53-81 <HUA>					
R;Tsugita, A.; Takamoto, K.; Kamo, M.; Iwadate, H.					
Eur. J. Biochem. 205, 691-696, 1992					
A;Title: C-terminal sequencing of protein. A novel partial acid hydrolysis and analysis					
A;Reference number: S23188; MUID:92298996; PMID:1606956					
A;Accession: S23309					
A;Molecule type: protein					
A;Residues: 53-81 <SU>					
C;Comment: In pancreatic alpha-cells, proglucagon is processed to truncated glucagon-like peptide 1, glucagon-stimulatory L cells, proglucagon is processed to truncated glucagon-like peptide 1, glucagon-					
dulin.					
A;Genes: GBB;GCG					
A;Cross-references: GDB:119265; OMIM:138030					
A;Map position: 2q36.2q37					
A;Introns: 31/2; 85/2; 131/2; 179/2					
<b>RESULT 2</b>					
glucagon precursor [validated] - human					
N;Contains: glicentin; glicentin-related polypeptide (GRPP); glucagon; glucagon-like peptide 1 (GICP1)					
C;Species: Homo sapiens (man)					
C;Date: 24-Apr-1984 #sequence_revision 31-Mar-1993 #text_change 08-Dec-2000					
C;Accession: A24377; R44197; A30875; A32614; A01541; S23509					
R;White, J.W.; Saunders, G.F.					
Nucleic Acids Res. 14: 4719-4730, 1986					
A;Title: Structure of the human glucagon gene.					
A;Reference number: A24377; MUID:86259053; PMID:3125587					
A;Accession: A24377					
A;Molecule type: DNA					
A;Residues: 1-180 <WH1>					
A;Cross-references: GB:X03991					
R;Bell, G.I.; Sanchez-Pescador, R.; Laybourn, P.J.; Nadrian, R.C.					
Nature 244, 368-371, 1983					
A;Title: Exon duplication and divergence in the human preproglucagon gene.					
A;Reference number: A44197; MUID:83271477; PMID:6877358					
A;Accession: A44197					
A;Residues: 1-179 <BEL2>					
A;Cross-references: GB:V01515; NID:931777; PIDN:CAA24759.1; PID:931778					
A;Molecule type: DNA					
A;Accession: A30875					
R;Drucker, D.J.; Asa, S.					
J. Biol. Chem. 263, 13475-13478, 1988					
A;Title: Glucagon gene expression in vertebrate brain					
A;Reference number: A30875; MUID:88330860; PMID:2901414					
A;Accession: A30875					
A;Molecule type: mRNA					
A;Residues: 1-180 <DRD>					
A;Cross-references: GB:J04040; NID:182029; PIDN:BAA2567.1; PID:183270					
R;Orskov, C.; Bersani, M.; Johansen, A.H.; Hojrup, P.; Holst, J.J.					
J. Biol. Chem. 264, 12826-12829, 1989					
A;Title: Complete sequences of glucagon-like peptide-1 from human and pig small intestine					
A;Reference number: A92732; MUID:89327238; PMID:253890					
A;Accession: A32614					
A;Molecule type: protein					
A;Residues: 98-127 <CRS>					
R;Thomsen, J.; Kristiansen, K.; Brunfeldt, K.; Sundby, F.					
FEBs Lett. 21, 315-319, 1972					
A;Title: The amino acid sequence of human glucagon.					
A;Reference number: A91373					
A;Accession: A01541					
A;Molecule type: protein					
A;Residues: 53-81 <HUA>					
R;Tsugita, A.; Takamoto, K.; Kamo, M.; Iwadate, H.					
Eur. J. Biochem. 205, 691-696, 1992					
A;Title: C-terminal sequencing of protein. A novel partial acid hydrolysis and analysis					
A;Reference number: S23188; MUID:92298996; PMID:1606956					
A;Accession: S23309					
A;Molecule type: protein					
A;Residues: 53-81 <SU>					
C;Comment: In pancreatic alpha-cells, proglucagon is processed to truncated glucagon-like peptide 1, glucagon-stimulatory L cells, proglucagon is processed to truncated glucagon-like peptide 1, glucagon-					
dulin.					
A;Genes: GBB;GCG					
A;Cross-references: GDB:119265; OMIM:138030					
A;Map position: 2q36.2q37					
A;Introns: 31/2; 85/2; 131/2; 179/2					
<b>RESULT 3</b>					
glucagon precursor - guinea pig					
N;Alternate names: oxyntomodulin					
C;Species: Cavia porcellus (guinea pig)					
C;Date: 30-Sep-1987 #sequence_revision 31-Dec-1992 #text_change 16-Jun-2000					
C;Accession: A24856; A23849; A60233					
R;Seino, S.; Welsh, M.; Bell, G.I.; Chan, S.J.; Steiner, D.F.					
FEMS Lett. 203, 25-30, 1986					
A;Title: Mutations in the guinea pig preproglucagon gene are restricted to a specific					
A;Reference number: A24856; MUID:86248118; PMID:3755107					
A;Accession: A24856					
A;Molecule type: mRNA					
A;Residues: 1-180 <SEI>					
A;Cross-references: DDBJ:D00014; GB:N00014; NID:9220288; PIDN:BAA00010.1; PID:9220289					
R;Huang, C.G.; Eng, J.; Pan, Y.C.E.; Holmes, J.D.; Yallow, R.S.					
Diabetes 35, 508-512, 1986					
A;Title: Guinea pig glucagon differs from other mammalian glucagons.					
A;Reference number: A22849; MUID:86165412; PMID:3956884					
A;Accession: A23849					
A;Molecule type: protein					
A;Residues: 53-81 <HUA>					
R;Conlon, J.M.; Hansen, H.F.; Schwartz, T.W.					
Regul. Pept. 11, 309-320, 1985					
A;Title: Primary structure of glucagon and a partial sequence of oxyntomodulin (gluca					
A;Reference number: A60323; MUID:86017849; PMID:4048553					
A;Accession: A60323					
A;Molecule type: protein					
A;Residues: 53-81 <CON>					
A;Note: glucagon-37 was not completely sequenced					
C;Superfamily: glucagon					
C;Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; pan					
F;1-20/Domain: signal sequence #status predicted <SIG>					
F;21-180/Product: proglucagon #status experimental <PGC>					
F;21-50/Region: glicentin-related peptide #status predicted					
F;53-89/Product: glucagon-37 (oxyntomodulin) #status experimental <GC37>					
F;98-127/Product: glucagon-like peptide 1 #status predicted <GLI>					
F;146-178/Product: glucagon-like peptide 2 #status predicted <GL2>					
F;127/Modified site: amidated carboxyl end (Arg) (amide in mature form from following					
Query Match 100.0%; Score 144; DB 1; Length 180;					
Best Local Similarity 100.0%; Pred. No. 1.3e-13; Mismatches 0; Indels 0; Gaps 0;					
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
<b>Qy</b>	1	HAEGETTSVDVSYLEGGAAKEFTIWLWIK	28		
<b>Db</b>	98	HAEGETTSVDVSYLEGGAAKEFTIWLWIK	125		

## RESULT 4

GCRD TU

glucagon precursor - degu

N; Contains: glicentin-related peptide; glucagon; glucagon-like peptide 1; glucagon-like

C; Species:

C; Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 18-Jun-1999

C; Accession: C36118

R; Nishi, M.; Steiner, D.F.

Mol: Endocrinol. 4, 1192-1198, 1990

A; Title: Cloning of complementary DNAs encoding islet amyloid polypeptide, insulin, and

A; Reference number: A36118; MUID:91155952; PMID:2293024

A; Accession: C36118

A; Molecule type: mRNA

A; Residues: 1-180 &lt;NIS&gt;

A; Cross-references: GB:M57688; NID:9202467; PIDN:AAA40588.1; PID:g202468

C; Superfamily: glucagon

C; Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; pancre

C; 1-20/Domain: signal sequence #status predicted &lt;SIG&gt;

F; 21-180/Product: proglucagon #status predicted &lt;PGC&gt;

F; 53-81/Region: glicentin-related peptide #status predicted

C; Species: Mesocricetus auratus (golden hamster)

C; Date: 13-Jun-1983 #sequence\_revision 13-Jun-1983 #text\_change 20-Mar-1998

C; Accession: A01539

R; Bell, G.I.; Santarre, R.F.; Mullerbach, G.T.

Nature 302, 716-718, 1983

A; Title: Hamster preproglucagon contains the sequence of

A; Reference number: A01539; MUID:83167563; PMID:6835407

A; Accession: A01539

A; Molecule type: mRNA

A; Residues: 1-180 &lt;BEL&gt;

A; Cross-references: EMBL:J00059

C; Superfamily: glucagon

C; 1-20/Domain: signal sequence #status predicted &lt;SIG&gt;

F; 21-180/Product: proglucagon #status predicted &lt;PGC&gt;

F; 53-81/Region: glicentin-related peptide #status predicted

C; Species: Bos primigenius taurus (cattle)

C; Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 20-Mar-1998

C; Accession: A93570; A92081; A01538

R; Lopez, L.C.; Frazier, M.L.; Su, C.J.; Kumar, A.; Saunders, G.F.

Proc. Natl. Acad. Sci. U.S.A. 80, 5485-5489, 1983

A; Title: Mammalian pancreatic preproglucagon contains three glucagon-related peptides

A; Reference number: A93570; MUID:83299996; PMID:6577439

A; Accession: A93570

A; Molecule type: mRNA

A; Residues: 1-180 &lt;LOP&gt;

A; Cross-references: EMBL:K00107

R; Brömer, W.W.; Boucher, M.E.; Koffenberger Jr., J.E.

J. Biol. Chem. 246, 2822-2827, 1971

A; Title: Amino acid sequence of bovine glucagon

A; Reference number: A92081; MUID:71166445; PMID:5102927

A; Accession: A92081

A; Molecule type: protein

A; Residues: 53-81 &lt;BRO&gt;

C; Superfamily: glucagon

F; 1-20/Domain: signal sequence #status predicted &lt;SGN&gt;

C; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-180 &lt;H22&gt;

A; Cross-references: GB:K02809; GB:K02810; GB:K02811; GB:K02812

C; Genetics

A; Introns: 31/2; 85/2; 131/2; 17/9/2

C; Superfamily: glucagon

C; Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; pancre

F; 1-20/Domain: signal sequence #status predicted &lt;SGN&gt;

C; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-180 &lt;H22&gt;

A; Cross-references: GB:K02809; GB:K02810; GB:K02811; GB:K02812

C; Genetics

A; Introns: 31/2; 85/2; 131/2; 17/9/2

C; Superfamily: glucagon

F; 1-20/Domain: signal sequence #status predicted &lt;SGN&gt;

C; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-180 &lt;H22&gt;

F; 21-180/Product: proglucagon #status predicted <PGC>  
 F; 21-180/Region: glicentin-related peptide #status predicted  
 F; 53-81/Region: glicentin-related peptide #status predicted <CCN>  
 F; 98-127/Product: glucagon-like peptide 1 #status predicted <GL1>  
 F; 146-180/Product: glucagon-like peptide 2 #status predicted <GL2>  
 F; 127/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl  
 Query Match 100.0%; Score 144; DB 1; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 1. 3e-13;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HAEGTFPSDVSSYLEGQAKERIATWLVK 28  
 Db 98 HAEGTFPSDVSSYLEGQAKERIATWLVK 125

Nature 302, 716-718, 1983  
 A; Title: Hamster preproglucagon contains the sequence of glucagon and two related pep  
 A; Reference number: A01539; MUID:83167563; PMID:6835407  
 A; Accession: A01539  
 A; Molecule type: mRNA  
 A; Residues: 1-180 <BEL>  
 A; Cross-references: EMBL:J00059  
 C; Superfamily: glucagon  
 C; 1-20/Domain: signal sequence #status predicted <SIG>  
 F; 21-180/Product: proglucagon #status predicted <PGC>  
 F; 53-81/Region: glicentin-related peptide #status predicted <CCN>  
 F; 98-127/Product: glucagon-like peptide 1 #status predicted <GL1>  
 F; 146-180/Product: glucagon-like peptide 2 #status predicted <GL2>  
 F; 127/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl  
 Query Match 100.0%; Score 144; DB 1; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 1. 3e-13;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HAEGTFPSDVSSYLEGQAKERIATWLVK 28  
 Db 98 HAEGTFPSDVSSYLEGQAKERIATWLVK 125

Nature 302, 716-718, 1983  
 A; Title: Hamster preproglucagon contains the sequence of glucagon and two related pep  
 A; Reference number: A01539; MUID:83167563; PMID:6835407  
 A; Accession: A01539  
 A; Molecule type: mRNA  
 A; Residues: 1-180 <BEL>  
 A; Cross-references: EMBL:J00059  
 C; Superfamily: glucagon  
 C; 1-20/Domain: signal sequence #status predicted <SIG>  
 F; 21-180/Product: proglucagon #status predicted <PGC>  
 F; 53-81/Region: glicentin-related peptide #status predicted <CCN>  
 F; 98-127/Product: glucagon-like peptide 1 #status predicted <GL1>  
 F; 146-180/Product: glucagon-like peptide 2 #status predicted <GL2>  
 F; 127/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl  
 Query Match 100.0%; Score 144; DB 1; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 1. 3e-13;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C:Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; pancreas  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-180/Product: proglucagon #status predicted <PGC>  
 F:21-50/Region: glucagon-related peptide #status predicted  
 F:23-81/Product: glucagon #status experimental <GCN>  
 F:23-151/Product: proglucagon #status predicted <PGC>  
 F:55-83/Product: glucagon #status experimental <GL1>  
 F:118-178/Product: glucagon-like peptide 2 #status predicted <GL2>  
 F:147/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gln)  
 F:147/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gln)

Query Match 100.0%; Score 144; DB 1; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 1 3e-13;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 HAEGTFTSDVSSYLEGQAKEFIAWLV 28  
 Db 98 HAEGTFTSDVSSYLEGQAKEFIAWLV 125

## RESULT 8

A57294

glicagon precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 01-Dec-1995 #sequence\_revision 01-Dec-1995 #text\_change 16-Jul-1999

C:Accession: A57294; S49903

R:Rothenberg, M.E.; Elterton, C.D.; Klein, K.; Zhou, Y.; Lindberg, I.; McDonald, J.K.;  
 J. Biol. Chem. 270, 10136-10146, 1995

A:Title: Processing of mouse proglucagon by recombinant prohormone convertase 1 and immu-

A:Reference number: A57294; MUID:95247722; PMID:7730317

A:Accession: A57294

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-180 <ROT>

A:Cross-references: EMBL:246845; NID:959980; PIDN:CAA86902.1; PID:9599801

C:Superfamily: glucagon

C:Keywords: carbohydrate metabolism; duplication; hormone; pancreas

Query Match 100.0%; Score 144; DB 2; Length 180;  
 Best Local Similarity 100.0%; Pred. 1 3e-13;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HAEGTFTSDVSSYLEGQAKEFIAWLV 28  
 Db 98 HAEGTFTSDVSSYLEGQAKEFIAWLV 125

## RESULT 9

GCCH

glucagon precursor - chicken

N:Contains: glucagon; glucagon-like peptide 1

C:Species: Gallus gallus (chicken)

C:Date: 31-Dec-1991 #sequence\_revision 31-Mar-1993 #text\_change 18-Jun-1999

C:Accession: S09992; A92189; A60836; A01442

R:Hasedawa, S.; Terakawa, K.; Natta, K.; Takada, T.; Yamamoto, H.; Okamoto, H.

FEBS Lett. 264, 117-120, 1990

A:Title: Nucleotide sequence determination of chicken glucagon precursor cDNA. Chicken

A:Reference number: S09992; MUID:90249492; PMID:2338135

A:Molecule type: mRNA

A:Residues: 1-151 <HAS>

A:Cross-references: EMBL:Y07539; NID:963749; PIDN:CAA68927.1; PID:963750

A:Molecule type: mRNA

A:Residues: 1-151 <HAS>

A:Title: Chicken glucagon. Isolation and amino acid sequence studies.

A:Reference number: A92189; MUID:76069271; PMID:1194290

A:Molecule type: protein

A:Residues: 55-83 <POX>

R:Biolk, H.G.; Kimmel, J.R.  
 J. Biol. Chem. 250, 9377-9380, 1975

A:Title: Chicken glucagon. Isolation and amino acid sequence studies.

A:Reference number: A92189; MUID:76069271; PMID:1194290

A:Accession: A60836

A:Molecule type: protein

A:Residues: 55-83 <POX>

R:Huang, J.; Eng, J.; Yallow, R.S.; Horm. Metab. Res. 19, 542-544, 1987

A:Title: Chicken glucagon: sequence and potency in receptor assay.

A:Reference number: A60836; MUID:88113418; PMID:2828209

A:Accession: A60836

A:Molecule type: protein

## RESULT 10

I51301

proglucagon - chicken

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999

C:Accession: I51301

R:Irwin, D.M.; Wong, J.

Mol. Endocrinol. 9, 267-277, 1995

A:Title: Trout and chicken proglucagon: alternative splicing generates mRNA transcript

A:Reference number: A55895; MUID:95295739; PMID:776976

A:Accession: I51301

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-205 <ROT>

A:Cross-references: GB:S78477; NID:999386; PIDN:AAB34506.1; PID:999387

C:Superfamily: glucagon

C:Keywords: duplication

Query Match 91.7%; Score 132; DB 2; Length 206;  
 Best Local Similarity 88.9%; Pred. 8 5e-12;  
 Matches 24; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HAEGTFTSDVSSYLEGQAKEFIAWLV 27  
 Db 118 HAEGTYTSDVSSYLEGQAKEFIAWLV 144

## RESULT 11

B61125

glucagon-like peptide - American eel

C:Species: Anguilla rostrata (American eel)

C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 21-Nov-1997

C:Accession: B61125

R:Conlon, J.M.; Andrews, P.C.; Thim, L.; Moon, T.W.

Gen. Comp. Endocrinol. 82, 23-32, 1991

A:Title: The primary structure of glucagon-like peptide but not insulin has been cons

A:Reference number: A61125; MUID:91340068; PMID:1874385

A:Molecule type: protein

A:Residues: 1-30 <CON>

A:Molecule type: protein

A:Accession: B61125

A:Residues: 1-30 <CON>

C:Superfamily: glucagon

C:Keywords: amidated carboxyl end; duplication

F:1-30/Product: glucagon-like peptide #status experimental <GLP>

F:30/Modified site: amidated carboxyl end (Arg) #status predicted

Query Match 81.9%; Score 118; DB 2; Length 30;

Best Local Similarity 80.9%; Pred. 1 2e-10;

Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HAEGTFTSDVSSYLEGQAKEFIAWL 26

Db 1 HAEGTYTSDVSSYLEGQAKEFVWL 26

## RESULT 12

c61125  
glucagon-like peptide - European eel  
C;Species: Anguilla anguilla (European eel)  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 21-Nov-1997  
C;Accession: C61125  
R;Conton, J.M.; Andrews, P.C.; Thim, L.; Moon, T.W.  
A;Title: The primary structure of glucagon-like peptide but not insulin has been conserv  
A;Reference number: A61125; MUID:91340068; PMID:1874385  
A;Accession: C61125  
A;Molecule type: protein  
A;Residues: 1-30 <CON>  
C;Superfamily: glucagon  
C;Keywords: amidated carboxyl end; duplication  
F;1-30/Product: glucagon-like peptide #status experimental <GLP>  
F;30/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match      Best Local Similarity 80.8%; Score 118; DB 2; Length 30;  
Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      1 HAEGTFPSDVSSELEGOAKERFIawl 26  
Db      |||||||:||||||:||||:|||  
1 HAEGTFTSDVSSELEGOAKERFIawl 26

RESULT 13  
GCFGB  
glucagon precursor - bullfrog (fragments)  
N;Alternate names: oxyntomodulin  
N;Contains: glucagon; glucagon-36 (oxyntomodulin); glucagon-like peptide 1; glucagon-lik  
C;Species: Rana catesbeiana (bullfrog)  
C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 20-Mar-1998  
C;Accession: B28091; C28091; D28091  
R;Pollock, H.G.; Hamilton, J.W.; Rouse, J.B.; Ebner, K.E.; Rawitch, A.B.  
J; Biol. Chem. 263, 9746-9751, 1988  
A;Title: Isolation of peptide hormones from the pancreas of the bullfrog (Rana catesbeia  
A;Reference number: A92730; MUID:88257102; PMID:3260236  
A;Molecule type: protein  
A;Residues: 1-36 <PO2>  
A;Accession: C28091  
A;Molecule type: protein  
A;Residues: 37-68 <PO2>  
A;Accession: D28091  
A;Molecule type: protein  
A;Residues: 69-101 <PO3>  
C;Superfamily: glucagon  
C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas  
F;1-36/Product: glucagon-36 (oxyntomodulin) #status experimental <GL3>  
F;1-29/Product: glucagon #status predicted <SIG>  
F;37-67/Product: glucagon-like peptide 1 #status experimental <GL1>  
F;69-101/Product: glucagon-like peptide 2 #status experimental <GL2>

Query Match      Best Local Similarity 81.9%; Score 118; DB 1; Length 30;  
Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy      1 HAEGTFPSDVSSELEGOAKERFIawl 28  
Db      |||||||:||||:||||:|||  
1 HAEGTFTSDVSSELEGOAKERFIawl 28  
Db      |||||||:||||:||||:|||  
1 HAEGTFTSDVSSELEGOAKERFIawl 64

RESULT 14  
GCIDC  
glucagon precursor - channel catfish (fragments)  
C;Species: Ictalurus punctatus (channel catfish)  
C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 20-Mar-1998  
C;Accession: A05166; A05167  
R;Andrews, P.C.; Ronner, P.  
J; Biol. Chem. 260, 3910-3914, 1985  
A;Title: Isolation and structures of glucagon and glucagon-like peptide from catfish par  
A;Reference number: A92514; MUID:85157536; PMID:38388546

A;Accession: A05166  
A;Molecule type: protein  
A;Residues: 1-29 <ANB1>  
A;Accession: A05167  
A;Molecule type: protein  
A;Residues: 30-63 <ANB2>  
C;Superfamily: glucagon  
C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas  
F;1-29/Product: glucagon #status experimental <GCN>  
F;30-63/Product: glucagon-like peptide 1 #status experimental <GL1>

Query Match      Best Local Similarity 76.9%; Score 112; DB 1; Length 63;  
Matches 20; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      1 HAEGTFTSDVSSELEGOAKERFIawl 26  
Db      |||||||:||||||:||||:|||  
1 HAEGTFTSDVSSELEGOAKERFIawl 26

RESULT 15  
GCAT2  
glucagon 2 precursor - American goosefish  
N;Contains: glucagon; glucagon-like peptide 1  
C;Species: Lophius americanus (American goosefish)  
C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 21-Jul-2000  
R;Lund, P.K.; Goodman, R.H.; Montminy, M.R.; Dee, P.C.; Habener, J.F.  
J; Biol. Chem. 258, 3280-3284, 1983  
A;Title: Anglerfish islet pre-proglucagon II. Nucleotide and corresponding amino acid  
A;Accession: A05150  
A;Residues: 1-122 <LUN>  
A;Molecule type: mRNA  
A;Cross-references: GB:J00933; NID:964021; PIDN:CAA23905.1; PID:964022  
C;Superfamily: glucagon  
C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas  
F;1-21/Domain: signal sequence  
F;22-122/Domain: proglucagon 2 #status predicted <PGC2>  
F;52-80/Product: glucagon #status predicted <CCN>  
F;89-119/Product: glucagon-like peptide 1 #status predicted <GL1>

Query Match      Best Local Similarity 73.1%; Score 112; DB 1; Length 122;  
Matches 19; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy      1 HAEGTFTSDVSSELEGOAKERFIawl 26  
Db      |||||||:||||||:||||:|||  
1 HAEGTFTSDVSSELEGOAKERFIawl 114

Search completed: March 19, 2003, 12:11:56  
Job time : 16 secs

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### OM protein - protein search, using sw model

Run on: March 19, 2003, 12:06:27 ; Search time 12 Seconds

(without alignments)  
96.778 Million cell updates/sec

Title: US-09-508-083-1

perfect score: 144

Sequence: 1 HAEGRFTSDVSYLEGQAAKEFTIAWLVK 28

### Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

### Database : Swissprot\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	144	100.0	158	1 GLUC_PIG	P01274 sus scrofa
2	144	100.0	180	1 GLUC_BOVIN	P01272 bos taurus
3	144	100.0	180	1 GLUC_CAVPO	P0110 cavia porce
4	144	100.0	180	1 GLUC_HUMAN	P01275 homo sapien
5	144	100.0	180	1 GLUC_MESAU	P01273 mesocricetus
6	144	100.0	180	1 GLUC_MOUSE	P5095 mus musculus
7	144	100.0	180	1 GLUC_OCTODE	P22890 octodon deg
8	144	100.0	180	1 GLUC_RAT	P00883 rattus norvegicus
9	132	91.7	151	1 GLUC_CHICK	P01277 gallus gallus
10	118	81.9	30	1 GLUM_ANGAN	P1521 anguilla anguilla
11	118	81.9	103	1 GLUC_RANCA	P15438 rana catesbeiana
12	112	77.8	122	1 GLU2_LOPAM	P0402 lophius americanus
13	111	77.1	71	1 GLUC_ICTPU	P0409 ictalurus punctatus
14	110	76.4	78	1 GLUC_LEPESP	P03566 lepisosteus osseus
15	109	75.7	71	1 GLUC_PIAME	P83880 piaractus maculatus
16	105	72.9	121	1 GLUC_CARRU	P79695 carassius carassius
17	104	72.2	68	1 GLUC_ONCKI	P0449 oncorhynchus
18	102.5	71.2	33	1 GLUC_ORENT	P83027 oreochromis
19	97	67.4	29	1 GLUC_TORMA	P09567 torpedo marmorata
20	97	67.4	96	1 GLUC_MYOSC	P03686 myoxocephalus thompsoni
21	95	66.0	29	1 GLUC_SCYCA	P05687 scylliorhinus stellaris
22	93	64.6	29	1 GLUC_CALMI	P13189 callobranchus
23	93	64.6	124	1 GLUC_LOPAM	P01278 lophius americanus
24	90	62.5	29	1 GLUC_DIDMA	P18108 didelphis marsupialis
25	90	62.5	29	1 GLUC_LAMPL	Q99rg9 lampetra fluviatilis
26	90	62.5	29	1 GLUC_RABIT	P2449 oryctolagus cuniculus
27	90	62.5	69	1 GLUC_CANFIA	P2794 canis familiaris
28	88	61.1	29	1 GLUC_ANAPL	P01276 anas platyrhynchos
29	88	61.1	36	1 GLUI_ORIENT	P81026 oreochromis
30	87	60.4	29	1 GLUC_CHTIRE	P33297 chinchilla laniger
31	86	59.7	29	1 GLUC_PLATE	P23062 platichthys
32	83	57.6	75	1 GLUC_AMICA	P3528 amia calva
33	83	57.6	1	EXE4_HELSU	P26349 heloderma suspectum

RESULT 1	GLUC_PIG	STANDARD:	PRN;	158 AA.
ID	GLUC_PIG			
AC	P01274;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Glucagon precursor. [Contains: Glicentin; Glicentin-related polypeptide (GPP); Glucagon; Glucagon-like Peptide 1 (GLP1); Glucagon-like peptide 2 (GLP2)] (Fragment).			
DE				
GN				
GGC.				
OS	Sus scrofa (Pig).			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCTI_TAXID=9623;			
RN	[1]			
RP	SEQUENCE OF 1-69.			
RX	MEDLINE:81248172; PubMed=6894800;			
RA	Thim L., Moody A.J.;			
RT	"The primary structure of porcine glicentin (proglucagon)."; Regul. Pept. 2:139-150(1981).			
RL	[2]			
RP	SEQUENCE OF 1-69.			
RX	MEDLINE:82221776; PubMed=7045833;			
RA	Thim L., Moody A.J.;			
RT	"The amino acid sequence of porcine glicentin.>"; Peptides 2 Suppl. 2:37-39(1981).			
RL	[3]			
RN	SEQUENCE OF 33-61.			
RP	MEDLINE:893238; PubMed=2753890;			
RA	Bromer W.W., Sinn L.G., Behrens O.K.;			
RT	"The amino acid sequence of glucagon. V. Location of amide groups, acid degradation studies and summary of sequential evidence.>"; J. Am. Chem. Soc. 79:2807-2810(1957).			
RL	[4]			
RP	SEQUENCE OF 78-107.			
RX	MEDLINE:893238; PubMed=2753890;			
RA	Orskov C., Bersani M., Johnsen A.H., Hoejrup P., Holst J.J.;			
RT	"Complete sequences of glucagon-like peptide-1 from human and pig RT small intestine.>"; J. Biol. Chem. 264:12826-12829(1989).			
RL	[5]			
RN	SEQUENCE OF 111-158.			
RP	MEDLINE:88243712; PubMed=3379036;			
RA	Bull T., Thim L., Kofod H., Orskov C., Harling H., Holst J.J.;			
RT	"Naturally occurring products of proglucagon 111-160 in the porcine and human small intestine.>"; J. Biol. Chem. 263:8621-8624(1988).			
RL	[6]			
X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).				
RX	MEDLINE:7605297; PubMed=171582;			
RA	Sasaki K., Dockett I.S., Adamik D.A., Tickle I.J., Blundell T.L.;			
RT	"X-ray analysis of glucagon and its relationship to receptor binding.>"; Nature 257:751-757(1975).			
RL				
CC	RAISES THE BLOOD SUGAR LEVEL.			

CC -1 FUNCTION: GLP2 STIMULATES INTESTINAL GROWTH AND UPREGULATES VILLUS  
 CC HEIGHT IN THE SMALL INTESTINE; CONCOMITANT WITH INCREASED CRYPT  
 CC CELL PROLIFERATION AND DECREASED ENTEROCYTE APOPTOSIS.  
 CC .-1 INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS  
 CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.  
 CC -1 MISCELLANEOUS: X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH  
 CC HUMAN SEQUENCE.  
 CC .-1 SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.  
 DR PIR: A01540; GCPG.  
 DR PDB: 1GCN; 30-SEP-83.  
 DR InterPro: IPR00532; Glucagon.  
 DR Pfam: PF00123; hormone2; 3.  
 DR SMART: SM00070; GLUCA; 3.  
 DR PROSITE: PS00260; GLUCAGON; 3.  
 KW Glucagon family; Hormone; Cleavage on pair of basic residues;  
 KW 3D-structure.  
 FT NON-TER 1 1  
 FT PEPTIDE 1 69 GLICENTIN.  
 FT PEPTIDE 1 30 GLICENTIN-RELATED POLYPEPTIDE.  
 FT PEPTIDE 33 61 GLUCAGON.  
 FT PEPTIDE 78 107 GLUCAGON-LIKE PEPTIDE 1.  
 FT PEPTIDE 126 158 GLUCAGON-LIKE PEPTIDE 2.  
 FT HELIX 39 42  
 FT TURN 43 45  
 FT HELIX 46 55  
 FT TURN 56 57  
 SQ SEQUENCE 158 AA; 18212 MW; 28C6FCR257F33B2 CRC64;

Query Match 100.0%; Score 144; DB 1; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 6-e-14;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HAEGTFTSDVSSYLEGQAAKEFIAWLVK 28  
 Db 78 HAEGTFTSDVSSYLEGQAAKEFIAWLVK 105

RESULT 2

ID	GLUC_BOVIN	STANDARD:	PRT:	180 AA.
AC				
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last annotation update)			
DE	Glucagon precursor [Contains: Glicentin-related polypeptide (GRPP); Glucagon; Glucagon-like peptide 1 (GLP1); Glucagon-like peptide 2 (GLP2)].			
GGC				
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.			
OX	NCBL-TAXID=9913;			
[1]				
RN	SEQUENCE FROM N.A. MEDLINE=8329996; PubMed=657439;			
RX	Lopez L.C., Frader M.L., Su C.-J., Kumar A., Saunders G.F.; "Mammalian pancreatic preproglucagon contains three glucagon-related peptides"; Proc. Natl. Acad. Sci. U.S.A. 80:5485-5489(1983), [2]			
RN	SEQUENCE OF 53-81; MEDLINE=7116645; PubMed=5102927;			
RX	Bromer W.W., Boucher M.E., Koffenberger J.B. Jr.; "Amino acid sequence of bovine glucagon. I"; J. Biol. Chem. 246:2822-2827(1971).			
RN	[3] STRUCTURE BY NMR OF 53-81; MEDLINE=7116645; PubMed=6631957;			
RX	Braun W., Wider G., Lee K.H., Wuthrich K.; "Conformation of glucagon in a lipid-water interphase by 1H nuclear magnetic resonance"; J. Mol. Biol. 169:921-948(1983).			

CC -1 FUNCTION: GLUCAGON PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.  
 CC FUNCTION: GLP2 STIMULATES INTESTINAL GROWTH AND UPREGULATES VILLUS HEIGHT IN THE SMALL INTESTINE; CONCOMITANT WITH INCREASED CRYPT CELL PROLIFERATION AND DECREASED ENTEROCYTE APOPTOSIS.  
 CC .-1 INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.  
 CC .-1 SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.  
 DR PIR: A01540; GCPG.  
 DR PDB: 1GCN; 30-SEP-83.  
 DR InterPro: IPR00532; Glucagon.  
 DR Pfam: PF00123; hormone2; 3.  
 DR SMART: SM00070; GLUCA; 3.  
 DR PROSITE: PS00260; GLUCAGON; 3.  
 KW Glucagon family; Hormone; Cleavage on pair of basic residues;  
 KW 3D-structure.  
 FT NON-TER 1 1  
 FT PEPTIDE 1 69 GLICENTIN.  
 FT PEPTIDE 1 30 GLICENTIN-RELATED POLYPEPTIDE.  
 FT PEPTIDE 33 61 GLUCAGON.  
 FT PEPTIDE 78 107 GLUCAGON-LIKE PEPTIDE 1.  
 FT PEPTIDE 126 158 GLUCAGON-LIKE PEPTIDE 2.  
 FT HELIX 39 42  
 FT TURN 43 45  
 FT HELIX 46 55  
 FT TURN 56 57  
 SQ SEQUENCE 158 AA; 18212 MW; 28C6FCR257F33B2 CRC64;

Query Match 100.0%; Score 144; DB 1; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6-9e-14;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HAEGTFTSDVSSYLEGQAAKEFIAWLVK 28  
 Db 98 HAEGTFTSDVSSYLEGQAAKEFIAWLVK 125

RESULT 3

ID	GLUC_CAVPO	STANDARD:	PRT:	180 AA.
AC				
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last annotation update)			
DE	Glucagon precursor [Contains: Glicentin-related polypeptide (GRPP); Glucagon; Glucagon-37 (Oxyntomodulin); Glucagon-like peptide 1 (GLP1); Glucagon-like peptide 2 (GLP2)].			
GGC				
OS	Cavia porcellus (Guinea pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.			
OX	NCBL-TAXID=10141;			
RN	SEQUENCE FROM N.A. MEDLINE=86248118; PubMed=3755107;			
RX	Seino S., Welsh M., Bell G.I., Chan S.J., Steiner D.F.; "Mutations in the guinea pig preproglucagon gene are restricted to a specific portion of the prohormone sequence. I"; FEBS Lett. 203:25-30(1986).			
RN	[2] SEQUENCE OF 53-81; MEDLINE=86165412; PubMed=3956884;			
RX	Huang C.G., Bng J., Pan Y.-C.E., Holmes J.D., Yalow R.S.; "Guinea pig glucagon differs from other mammalian glucagons. II"; FEBS Lett. 235:508-512(1986).			
RN	[3] PARTIAL SEQUENCE OF 53-89.			

CC -1 FUNCTION: GLUCAGON PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.  
 CC FUNCTION: GLP2 STIMULATES INTESTINAL GROWTH AND UPREGULATES VILLUS HEIGHT IN THE SMALL INTESTINE; CONCOMITANT WITH INCREASED CRYPT CELL PROLIFERATION AND DECREASED ENTEROCYTE APOPTOSIS.  
 CC .-1 INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.  
 CC .-1 SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.  
 DR PIR: A01538; GCPG.  
 DR PDB: 1KX6; 13-FEB-02.  
 DR InterPro: IPR00532; Glucagon.  
 DR Pfam: PF00123; hormone2; 3.  
 DR SMART: SM00070; GLUCA; 3.  
 DR PROSITE: PS00260; GLUCAGON; 4.  
 KW Glucagon family; Hormone; Cleavage on pair of basic residues; Signal; 3D-structure.  
 FT SIGNAL 1 20  
 FT PEPTIDE 21 50 GLICENTIN-RELATED POLYPEPTIDE.  
 FT PEPTIDE 53 81 GLUCAGON.  
 FT PEPTIDE 92 128 GLUCAGON-LIKE PEPTIDE 1.  
 FT PEPTIDE 146 178 GLUCAGON-LIKE PEPTIDE 2.  
 SQ SEQUENCE 180 AA; 20944 MW; 8D984FF05B9F15FF CRC64;

Query Match 100.0%; Score 144; DB 1; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6-9e-14;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HAEGTFTSDVSSYLEGQAAKEFIAWLVK 28  
 Db 98 HAEGTFTSDVSSYLEGQAAKEFIAWLVK 125



KW Glucagon family; Hormone; Cleavage on pair of basic residues; Signal;

KW Pharmaceutical; 3D-structure.

FT SIGNAL 1 20 GLICENTIN-RELATED POLYPEPTIDE.

FT PEPTIDE 21 50 GLUCAGON-LIKE PEPTIDE.

FT PEPTIDE 53 81 GLUCAGON-LIKE PEPTIDE 1.

FT PEPTIDE 98 127 GLUCAGON-LIKE PEPTIDE 2.

FT PEPTIDE 146 178 GLUCAGON-LIKE PEPTIDE 2.

FT PEPTIDE 82 82 K -> N (IN REF. 3).

SQ SEQUENCE 180 AA: 20909 MW: 7499EEC629B2862C CRC64;

Query Match 100.0%; Score 144; DB 1; Length 180;  
Best Local Similarity 100.0%; Pred. No. 6 9e-14; Mismatches 0; Indels 0; Gaps 0;  
Matches 28; Conservative 0; MisMatches 0;

Qy 1 HAEGTFTSDVSSYLEGQAKEFIAWLKV 28  
Db 98 HAEGTFTSDVSSYLEGQAKEFIAWLKV 125

RESULT 5

GLUC\_MESAU STANDARD PRT: 180 AA.

ID GLUC\_MESAU STANDARD PRT: 180 AA.

AC P01273; Rel. 01, Created DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 21-JUL-1986 (Rel. 01, Created) DT 01-OCT-1996 (Rel. 34, Last sequence update)

DE Glucagon precursor [Contains: Glicentin-related polypeptide (GRPP); DE Glucagon; Glucagon-like peptide 1 (GLP1); Glucagon-like peptide 2 (GLP2)].

DE Glucagon; Glucagon-like peptide 2 (GLP2). DE GLC.

OS Mesocricetus auratus (Golden hamster). OS musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Crustacea; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC Mesocricetus. OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; OX NCBI\_TAXID=10036; OX NCBI\_TAXID=10090;

RN SEQUENCE FROM N.A. RN SEQUENCE FROM N.A.

RP MEDLINE=83167563; PubMed=6835407; RP TISSUE-Pancreatic islets;

RA Bell G.I., Santeure R.F., Mullerbach G.T.; RX MEDLINE=95247722; PubMed=7730317;

RT "Hamster preproglucagon contains the sequence of glucagon and two RA Rothenberg M.E., Ellertson C.D., Klein K., Zhou Y., Linberg I., McDonald J.K., Mackin R.B., Noe B.D.; RT Processing of mouse proglucagon by recombinant prohormone convertase 1 and immunopurified prohormone convertase 2 in vitro.";

RT Nature 302:716-718(1993). RL J. Biol. Chem. 270:10136-10146(1995).

RP SEQUENCE FROM N.A. RN [2]

RA Shamsadin R., Knebel W.; RT Mouse glucagon full length cDNA.;"

RP REVISIONS TO 12-15. RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

RA Bell G.I.; CC -1- FUNCTION: GLUCAGON PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND CC RAISES THE BLOOD SUGAR LEVEL.

CC -1- FUNCTION: GLP2 STIMULATES INTESTINAL GROWTH AND UPREGULATES VILLUS CC HEIGHT IN THE SMALL INTESTINE, CONCOMITANT WITH INCREASED CRYPT CC CELL PROLIFERATION AND DECREASED ENTEROCYTE APOPTOSIS.

CC -1- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

CC -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.

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CC ----- DR InterPro: IPR00532; Glucagon.

CC DR PRINTS: PR00275; GLUCAGON.

CC DR SMART: SM00070; GLUCA; 3.

CC DR PROSITE: PS00260; GLUCAGON; 4.

CC KW Glucagon family; Hormone; Cleavage on pair of basic residues; Signal.

FT SIGNAL 1 20 BY SIMILARITY.

FT PEPTIDE 1 20 GLICENTIN-RELATED POLYPEPTIDE.

FT PEPTIDE 21 50 GLUCAGON.

FT PEPTIDE 53 81 GLUCAGON-LIKE PEPTIDE 1.

FT PEPTIDE 98 127 GLUCAGON-LIKE PEPTIDE 2.

FT PEPTIDE 146 178 GLUCAGON-LIKE PEPTIDE 2.

FT PEPTIDE 82 82 K -> N (IN REF. 3).

SQ SEQUENCE 180 AA: 20954 MW: 02791B49D7AADD4B CRC64;

Query Match 100.0%; Score 144; DB 1; Length 180;  
Best Local Similarity 100.0%; Pred. No. 6 9e-14; Mismatches 0; Indels 0; Gaps 0;  
Matches 28; Conservative 0; MisMatches 0;

Qy 1 HAEGTFTSDVSSYLEGQAKEFIAWLKV 28  
Db 98 HAEGTFTSDVSSYLEGQAKEFIAWLKV 125

RESULT 6

GLUC\_MOUSE STANDARD PRT: 180 AA.

ID GLUC\_MOUSE STANDARD PRT: 180 AA.

AC P55095; DT 01-OCT-1996 (Rel. 34, Created)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Glucagon precursor [Contains: Glicentin-related polypeptide (GRPP); DE Glucagon; Glucagon-like peptide 1 (GLP1); Glucagon-like peptide 2 (GLP2)].

DE Glucagon; Glucagon-like peptide 2 (GLP2). DE GLC.

OS Mus musculus (Mouse). OS musculus (Mouse).

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; OX NCBI\_TAXID=10090;

RN [1]

RP SEQUENCE FROM N.A. RP TISSUE-Pancreatic islets;

RC MEDLINE=95247722; PubMed=7730317; RX MEDLINE=95247722; PubMed=7730317;

RA McDonald J.K., Mackin R.B., Noe B.D.; RA Rothenberg M.E., Ellertson C.D., Klein K., Zhou Y., Linberg I., McDonald J.K., Mackin R.B., Noe B.D.; RT Processing of mouse proglucagon by recombinant prohormone convertase 1 and immunopurified prohormone convertase 2 in vitro.";

RT J. Biol. Chem. 270:10136-10146(1995).

RN [2]

RP SEQUENCE FROM N.A. RA Shamsadin R., Knebel W.; RT Mouse glucagon full length cDNA.;"

RP REVISIONS TO 12-15. RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

RA Bell G.I.; CC -1- FUNCTION: GLUCAGON PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND CC RAISES THE BLOOD SUGAR LEVEL.

CC -1- FUNCTION: GLP2 STIMULATES INTESTINAL GROWTH AND UPREGULATES VILLUS CC HEIGHT IN THE SMALL INTESTINE, CONCOMITANT WITH INCREASED CRYPT CC CELL PROLIFERATION AND DECREASED ENTEROCYTE APOPTOSIS.

CC -1- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

CC -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.

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CC ----- DR InterPro: IPR00532; Glucagon.

CC DR PRINTS: PR00275; GLUCAGON.

CC DR SMART: SM00070; GLUCA; 3.

CC DR PROSITE: PS00260; GLUCAGON; 4.

CC KW Glucagon family; Hormone; Cleavage on pair of basic residues; Signal.

FT SIGNAL 1 20 BY SIMILARITY.

FT PEPTIDE 1 20 GLICENTIN-RELATED POLYPEPTIDE.

				Best Local Similarity	100.0%	Pred. No.	6.9e-14	Indels	0	Gaps	0
FT	PEPTIDE	53	81	GLUCAGON.							
FT	PEPTIDE	92	128	GLUCAGON-LIKE PEPTIDE 1.							
FT	PEPTIDE	146	178	GLUCAGON-LIKE PEPTIDE 2.							
SQ	SEQUENCE	180 AA;	20906 MW;	595A6DD9A58950 CRC64;							
Query Match		100.0%;	Score 144;	DB 1;	Length 180;						
Matches		28;	Conservative	0;	Mismatches						
Qy	1	HAEGTFSDVSSYLEGQAKEFIAWLVK	28								
Db	98	HAEGTFSDVSSYLEGQAKEFIAWLVK	125								
RESULT 7											
GUCL-OCTDE											
ID - GLUC-OCTDE											
STANDARD:											
PRT;											
180 AA.											
AC P22890;											
DT 01-AUG-1991 (Rel. 19, Created)											
DT 01-AUG-1991 (Rel. 19, Last sequence update)											
DT 16-OCT-2001 (Rel. 40, Last annotation update)											
DE Glucagon precursor [Contains: Glicentin-related polypeptide (GRPP); Glucagon; Glucagon-like peptide 1 (GLP1); Glucagon-like peptide 2 (GLP2); GCG.											
OS Octodon degus (Degu).											
OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Octodontidae; Octodon.											
OX NCBI_TAXID=10160;											
RN [1]											
RP .											
SEQUENCE FROM N_A.											
RX MEDLINE=9115955;											
RA Nishi M., Steiner D.F.;											
RT "Cloning of complementary DNAs encoding islet amyloid polypeptide, insulin, and glucagon precursors from a New World rodent, the degu, Octodon degus.";											
RL Mol. Endocrinol. 4:1192-1198 (1990).											
CC -1- FUNCTION: GLUCAGON PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.											
CC -!- FUNCTION: GLP2 STIMULATES INTESTINAL GROWTH AND UPREGULATES VILLUS HEIGHT IN THE SMALL INTESTINE, CONCOMITANT WITH INCREASED CRYPT CELL PROLIFERATION AND DECREASED ENTEROCYTE APOPTOSIS.											
CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.											
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.											
CC											
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CC											
EMBL: M57658; AAA440598.1; - .											
DR PIR; C36188; GCFIDU.											
DR HSSP; P01274; IGCN.											
DR InterPro; IPR000532; Glucagon.											
DR Pfam; PF00123; hormone2; 3.											
DR PRINTS; PR00275; GLUCAGON.											
DR SMART; SM00070; GLUCA; 3.											
DR PROSITE; PS00260; GLUCAGON; 4.											
KW Glucagon family; Hormone; Cleavage on pair of basic residues: Signal;											
FT SIGNAL 1 20											
FT PEPTIDE 21 50											
FT PEPTIDE 53 81											
FT PEPTIDE 92 127											
FT PEPTIDE 146 178											
FT MOD-RES 127 127											
SQ SEQUENCE 180 AA; 21165 MW; 6E836160A9A3031 CRC64;											
Query Match		100.0%;	Score 144;	DB 1;	Length 180;						

DR PRINTS; PRO0275; GLUCAGON.  
 DR SMART; SM0070; GLUCA; 3.  
 DR PROSITE; PS00260; GLUCAGON; 4.  
 KW Glucagon family; Hormone; Cleavage on pair of basic residues; Signal;  
 SIGNAL 1 20  
 FT PEPTIDE 21 50 GLICENTIN-RELATED POLYPEPTIDE.  
 FT PEPTIDE 53 81 GLUCAGON.  
 FT PEPTIDE 92 128 GLUCAGON-LIKE PEPTIDE 1.  
 FT PEPTIDE 146 178 GLUCAGON-LIKE PEPTIDE 2.  
 CC SEQUENCE 180 AA; 20846 MW; 76931409D03C7978 CRC4;  
 CC

Query Match 100.0%; Score 144; DB 1; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-14; Indels 0; Gaps 0;  
 Matches 28; Conservative 0; Mismatches 0;

OY 1 HAGTFTSDVSSYLEGQAKEFTAWLV 28  
 Db 98 HAGTFTSDVSSYLEGQAKEFTAWLV 125

RESULT 9  
 GLUC\_CHICK STANDARD; PRT; 151 AA.  
 ID GLUC\_CHICK STANDARD; PRT; 151 AA.  
 AC P01277;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-JUL-1995 (Rel. 38, Last annotation update)  
 DE Glucagon precursor.  
 OS Meleagris gallopavo (Chicken), and  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TAXID=9031, 9103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIESChicken; TISSUE=Pancreas;  
 RX MEDLINE=90249492; PubMed=233813eas;  
 RA Hasegawa S., Terazono K., Nata K., Takada T., Yamamoto H.,  
 RA Okamoto H.;  
 RT "Nucleotide sequence determination of chicken glucagon precursor  
 RNA. Chicken preproglucagon does not contain glucagon-like peptide  
 RT II";  
 FEBS Lett. 264:117-120(1990).  
 RN [2]  
 RP SEQUENCE OF 55-83.  
 RC SPECIESChicken;  
 RX MEDLINE=76059271; PubMed=1194290;  
 RA Pollock H.G., Kimmel J.R.;  
 RT "Chicken glucagon. Isolation and amino acid sequence studies.",  
 J. Biol. Chem. 250:9377-9380(1975).  
 RN [3]  
 RP COMPOSITION, AND SEQUENCE OF 55-83.  
 RC SPECIESGallopavo;  
 RX MEDLINE=73074118; PubMed=4645932;  
 RA Markussen J., Frandsen E.K., Hedding L.G., Sundby K.F.;  
 RT "Turkey glucagon: crystallization, amino acid composition and  
 immunology.",  
 RL Horm. Metab. Res. 4:360-363(1972).  
 CC -1- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES  
 THE BLOOD SUGAR LEVEL.  
 CC -1- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS  
 CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.  
 CC -1- MISCELLANEOUS: THE COMPOSITION OF TURKEY GLUCAGON APPEARS TO BE  
 CC IDENTICAL WITH CHICKEN.  
 CC -1- MISCELLANEOUS: CHICKEN PREPROGLUCAGON DOES NOT CONTAIN  
 CC GLUCAGON-LIKE PEPTIDE II.  
 CC -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.

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CC ---

CC EMBL; Y07539; CAA68827.1; -.  
 DR PIR; S05992; GCCH.  
 DR PIR; A91740; A91740.  
 DR HSSP; P01274; IGN; Glucagon.  
 DR InterPro; IPR000532; Glucagon.  
 DR Pfam; PF00123; hormone2; 2.  
 DR PRINTS; PRO0275; GLUCAGON.  
 DR SMART; SM0070; GLUCA; 2.  
 DR PROSITE; PS00260; GLUCAGON.  
 DR SMART; SM0070; GLUCA; 2.  
 DR PROSITE; PS00260; GLUCAGON; 3.  
 KW Glucagon family; Hormone; Cleavage on pair of basic residues; Signal;  
 SIGNAL 1 22  
 FT CHAIN 23 151 PROGLUCAGON.  
 FT PEPTIDE 55 83 GLUCAGON-LIKE PEPTIDE.  
 FT PROTEP 86 118 AMIDATION (G-148 PROVIDE AMIDE GROUP).  
 FT PEPTIDE 118 147 GLUCAGON.  
 FT MOD\_RES 147 151 AA; 17520 MW; B6CD087536C0AE5 CRC64;  
 SQ Sequence 151 AA; 17520 MW; B6CD087536C0AE5 CRC64;

Query Match 91.7%; Score 132; DB 1; Length 151;  
 Best Local Similarity 88.9%; Pred. No. 3.2e-12; Indels 0; Gaps 0;  
 Matches 24; Conservative 3; Mismatches 0;

OY 1 HAGTFTSDVSSYLEGQAKEFTAWLV 27  
 Db 118 HAGTFTSDVSSYLEGQAKEFTAWLV 144

RESULT 10  
 GLUM\_ANGAN STANDARD; PRT; 30 AA.  
 ID GLUM\_ANGAN STANDARD; PRT; 30 AA.  
 AC P41521;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Glucagon-like Peptide (GLP).  
 OS Anguilla anguilla (European freshwater eel), and  
 Anguilla rostrata (American eel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;  
 OX NCBI\_TAXID=7936, 7938;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=91340068; PubMed=1874385;  
 RA Conlon J.M., Andrews P.C., Thim L., Moon T.W.;  
 RT "The primary structure of glucagon-like peptide but not insulin has  
 been conserved between the American eel, *Anguilla rostrata* and the  
 European eel, *Anguilla anguilla*";  
 RT Gen. Comp. Endocrinol. 82:23-32(1991).  
 RL Comp. Endocrinol. 82:23-32(1991).  
 DR PIR; B61125; B61125.  
 DR PIR; C61125; C61125.  
 DR HSP; P01275; IBHO.  
 DR InterPro; IPR000532; Glucagon.  
 DR Pfam; PF00123; hormone2; 1.  
 DR PRINTS; PRO0275; GLUCAGON.  
 DR SMART; SM0070; GLUCA; 1.  
 DR PROSITE; PS00260; GLUCAGON; 1.  
 KW Glucagon family; Amidation.  
 FT MOD\_RES 30 30 AMIDATION.

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CC ---

CC Query Match 81.9%; Score 118; DB 1; Length 30;  
 CC Best Local Similarity 80.8%; Pred. No. 6.8e-11; Indels 0; Gaps 0;  
 CC Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 CC use by non-profit institutions as long as its content is in no way

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CC ---

CC EMBL; Y07539; CAA68827.1; -.  
 DR PIR; S05992; GCCH.  
 DR HSSP; P01274; IGN; Glucagon.  
 DR InterPro; IPR000532; Glucagon.  
 DR Pfam; PF00123; hormone2; 2.  
 DR PRINTS; PRO0275; GLUCAGON.  
 DR SMART; SM0070; GLUCA; 2.  
 DR PROSITE; PS00260; GLUCAGON; 3.  
 KW Glucagon family; Hormone; Cleavage on pair of basic residues; Signal;  
 SIGNAL 1 118  
 FT CHAIN 23 151 PROGLUCAGON.  
 FT PEPTIDE 55 83 GLUCAGON-LIKE PEPTIDE.  
 FT PROTEP 86 118 AMIDATION (G-148 PROVIDE AMIDE GROUP).  
 FT PEPTIDE 118 147 GLUCAGON.  
 FT MOD\_RES 147 151 AA; 17520 MW; B6CD087536C0AE5 CRC64;

Query Match 91.7%; Score 132; DB 1; Length 151;  
 Best Local Similarity 88.9%; Pred. No. 3.2e-12; Indels 0; Gaps 0;  
 Matches 24; Conservative 3; Mismatches 0;

OY 1 HAGTFTSDVSSYLEGQAKEFTAWLV 26

Db 1 HAEGTFTSDVSSYLOQAKEFVSWL 26  
**RESULT 11**  
 GLUC\_RANCA STANDARD; PRT; 103 AA.  
 ID GLUC\_RANCA STANDARD; PRT; 103 AA.  
 AC P15439; P15439; P15440;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE Glucagon precursor (Fragments).  
 OS Rana catesbeiana (Bull frog).  
 OC Bokai,Yota; Metacca; Choriatte; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE="Pancreas".  
 RX MEDLINE=8805710; PubMed=3260236;  
 RA Pollock, H.G.; Hamilton, J.W.; Rouse, J.B.; Ebner, K.E.; Rawitch, A.B.;  
 RT "Isolation of peptide hormones from the pancreas of the bullfrog,  
 (Rana catesbeiana). Amino acid sequences of pancreatic polypeptide,  
 oxyntomodulin, and two glucagon-like peptides.";  
 RT J. Biol. Chem. 263:9746-9751(1988).  
 CC -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES  
 THE BLOOD SUGAR LEVEL.  
 CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS  
 IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.  
 CC -!- MISCELLANEOUS: X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH  
 OTHER SPECIES SEQUENCES.  
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.  
 CC PIR: B28091; GCGB.  
 DR HSSP; P01274; IGCN.  
 DR InterPro; IPR000532; Glucagon.  
 DR Prints; PR00275; GLUCAGON.  
 DR SMART; SM00070; GLUCA; 3.  
 DR PROSITE; PS00260; GLUCAGON; 3.  
 DR KW Glucagon family; Hormone; Cleavage on pair of basic residues; Signal.  
 FT PEPTIDE 1 29 GLUCAGON.  
 FT PEPTIDE 1 36 GLUCAGON-36 (OXINTOMODULIN).  
 FT PEPTIDE 1 39 GLUCAGON-LIKE PEPTIDE 1.  
 FT PEPTIDE 1 70 GLUCAGON-LIKE PEPTIDE 2.  
 FT PEPTIDE 1 71 103 AA; 11719 MW; 316287B7BAE1C8F7 CRC64;  
 SQ Query Match 81.9%; Score 118; DB 1; Best Local Similarity 75.0%; Pred. No. 2.4e-10; Length 103; Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 HAEGTFTSDVSSYLOQAKEFVSWL 28  
 Db 39 HADGTTFSMDSSYLOQAKEFVSWL 66  
**RESULT 12**  
 GLU2\_LOPAM STANDARD; PRT; 122 AA.  
 ID GLU2\_LOPAM STANDARD; PRT; 122 AA.  
 AC P04092; P04092;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 01-NOV-1986 (Rel. 03, Last sequence update)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 01-NOV-1990 (Rel. 16, Last annotation update)  
 DE Glucagon II precursor [Contains: Glucentin-related polypeptide (GRPP);  
 DE Glucagon II; Glucagon-like peptide III].  
 OS Lophius americanus (American goosefish) (Anglerfish).  
 OC Bokai,Yota; Metacca; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;  
 OC Ictaluridae; Ictalurus.  
 OC Hoesein, N.M.; Mahrenholz, A.M.; Andrews, P.C.; Gurd, R.S.;  
 OC Biological activities of catfish glucagon and glucagon-like  
 peptide.;  
 RN Biochem. Biophys. Res. Commun. 143:87-92(1987).  
 RN SEQUENCE FROM N. A.  
 RX MEDLINE=83135785; PubMed=6338015;  
 RA Lund, P.K.; Goodman, R.H.; Montminy, M.R.; Dee, P.C.; Habener, J.F.;

RX MEDLINE=85157536; PubMed=3838546;  
 RA Andrews P.C., Ronner P.;  
 RT 'Isolation and structures of glucagon and glucagon-like peptide from  
 catfish pancreas';  
 RL J. Biol. Chem. 260:3910-3914(1985).  
 CC -I- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES  
 THE BLOOD SUGAR LEVEL.  
 -I- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS  
 IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.  
 -I- MISCELLANEOUS: X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH  
 AMERICAN GOOSEFISH SEQUENCES.  
 -I- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.  
 PRT; A05166; GCDC.  
 DR HSSP; P01274; IGCN.  
 DR InterPro; IPR000532; Glucagon.  
 DR Pfam; PF00123; hormone2; 2.  
 DR SMART; SM00070; GLUCA; 2.  
 DR PROSITE; PS00260; GLUCAGON; 2.  
 DR HSSP; P01274; IGCN.  
 DR InterPro; IPR000532; Glucagon.  
 DR Pfam; PF00123; hormone2; 2.  
 DR SMART; SM00070; GLUCA; 2.  
 DR PROSITE; PS00260; GLUCAGON; 2.  
 KW Glucagon family; Hormone.  
 FT NON\_TER 1 1  
 PEPTIDE 1 29  
 FT PEPTIDE 38 71  
 FT CONFLICT 53 53  
 FT NON\_TER 71 71  
 SQ SEQUENCE 71 AA: 8173 MW: 24688E79AD9B1A8F CRC64;  
 Query Match 77.1%; Score 111; DB 1; Length 71;  
 Best Local Similarity 76.9%; Pred. No. 1.7e-09;  
 Matches 20; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 HAEGTFPSDVSSYLEQAAKFTIAWL 26  
 ||:|||||:|||||:|||:|||:  
 Db 38 HADGTTSDVSSYLQEOAKDFITWL 63  
 ||:|||||:|||||:|||:|||:  
 RESULT 14  
 GLUC\_LBSP STANDARD; PRT; 78 AA.  
 ID GLUC\_LBSP  
 AC P09566;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Glucagon precursor [Contains: Glucagon; Glucagon-36 (Oxyntomodulin);  
 OS Lepisosteus spatula (Alligator gar) (Actrostostes spatula).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;  
 OC Lepisosteus  
 OX NCBI\_TaxID=7917;  
 RN [1]  
 RP SEQUENCE OF 1-36 AND 45-78.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=88196798; PubMed=3282974;  
 RA Pollock H.G., Kimmel J.R., Ebner K.E., Hamilton J.W., Rouse J.B.,  
 RA Lance V., Rawitch A.B.;  
 RT 'Isolation of alligator gar (Lepisosteus spatula) glucagon,  
 RT oxyntomodulin, and glucagon-like peptide amino acid sequences of  
 RT oxyntomodulin and glucagon-like peptide.';  
 RT Gen. Comp. Endocrinol. 69:133-140(1988).  
 RN [2]  
 RP PRELIMINARY SEQUENCE OF 1-29.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=88030594; PubMed=3311873;  
 RA Pollock H.G., Kimmel J.R., Hamilton J.W., Rouse J.B., Ebner K.E.,  
 RA Lance V., Rawitch A.B.;  
 RT 'Isolation and structures of alligator gar (Lepisosteus spatula)  
 RT insulin and pancreatic polypeptide.';  
 RL Gen. Comp. Endocrinol. 67:375-382(1987).  
 CC -I- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES  
 THE BLOOD SUGAR LEVEL.  
 CC -I- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS  
 CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.  
 CC -I- MISCELLANEOUS: X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH  
 CC AMERICAN GOOSEFISH SEQUENCES.  
 CC -I- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.  
 CC PRT; S06339; GCGA.  
 DR HSSP; P01274; IGCN.  
 DR InterPro; IPR000532; Glucagon.  
 DR Pfam; PF00123; hormone2; 2.  
 DR SMART; SM00070; GLUCA; 2.  
 DR PROSITE; PS00260; GLUCAGON; 2.  
 DR HSSP; P01274; IGCN.  
 DR InterPro; IPR000532; Glucagon.  
 DR Pfam; PF00123; hormone2; 2.  
 DR SMART; SM00070; GLUCA; 2.  
 DR PROSITE; PS00260; GLUCAGON; 2.  
 KW Glucagon family; Hormone.  
 FT PEPTIDE 1 29  
 FT PEPTIDE 38 71  
 FT NON\_TER 71 71  
 SQ SEQUENCE 71 AA: 8146 MW: 30106496271594 ED CRC64;  
 Query Match 76.4%; Score 110; DB 1; Length 78;  
 Best Local Similarity 73.1%; Pred. No. 2.6e-09;  
 Matches 19; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 HAEGTFPSDVSSYLEQAAKFTIAWL 26  
 Db 38 HADGTTSDVSSYLQEOAKDFITWL 63  
 ||:|||||:|||||:|||:|||:  
 RESULT 15  
 GLUC\_PIAME STANDARD; PRT; 71 AA.  
 ID GLUC\_PIAME  
 AC P01880;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE Glucagon precursor (Fragment).  
 OS Piaraactus mesopotamicus (Piactu).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Buteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Characiformes;  
 OC Characidae; Piaraactus.  
 OX NCBI\_TaxID=42528;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=99259587; PubMed=10327603;  
 RA de Lima J.A., Oliveira B., Conlon J.M.;  
 RT 'Purification and characterization of insulin and peptides derived  
 from piroglycagon and prosomatostatin from the fruit-eating fish, the  
 RT pacu Piaraactus mesopotamicus'.  
 RL Comp. Biochem. Physiol. 122B:27-135(1999).  
 CC -I- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES  
 CC THE BLOOD SUGAR LEVEL.  
 CC -I- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS  
 CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.  
 CC -I- MISCELLANEOUS: X'S IN THE SEQUENCE WERE INCLUDED BY HOMOLOGY WITH  
 CC OTHER FISH SEQUENCES.  
 CC -I- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.  
 DR InterPro; IPR000532; Glucagon.  
 DR Pfam; PF00123; hormone2; 2.  
 DR SMART; SM00070; GLUCA; 2.  
 DR PROSITE; PS00260; GLUCAGON; 2.  
 DR HSSP; P01274; IGCN.  
 DR InterPro; IPR000532; Glucagon.  
 DR Pfam; PF00123; hormone2; 2.  
 DR SMART; SM00070; GLUCA; 2.  
 DR PROSITE; PS00260; GLUCAGON; 2.  
 KW Glucagon family; Hormone.  
 FT NON\_TER 1 1  
 FT PEPTIDE 1 29  
 FT PEPTIDE 38 71  
 FT NON\_TER 71 71  
 SQ SEQUENCE 71 AA: 8146 MW: F66A3CA2DD9806C5 CRC64;  
 Query Match 75.3%; Score 109; DB 1; Length 71;  
 Best Local Similarity 73.4%; Pred. No. 3.4e-09;  
 Matches 19; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 HAEGTFPSDVSSYLEQAAKFTIAWL 26  
 Db 38 HADGTTSDVSSYLQEOAKDFITWL 63  
 ||:|||||:|||||:|||:|||:

Wed Mar 19 12:17:53 2003

us-09-508-083-1.rsp

Page 9

Search completed: March 19, 2003, 12:10:55  
Job time : 13 secs

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## ON protein - protein search, using sw model

Run on: March 19, 2003, 12:09:02 ; Search time 29 Seconds  
(without alignments)

US-09-508-083-1  
1 HAEQTFTSDVSSYLEGQAKEFIAWLVK 28  
198.942 Million cell updates/sec

## Title: Perfect score:

144 1 HAEQTFTSDVSSYLEGQAKEFIAWLVK 28

## Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

## Searched: 671580 seqs, 206047115 residues

## Total number of hits satisfying chosen parameters: 671580

## Minimum DB seq length: 0

## Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database : SPTRMBL\_21;\*

- 1: sp\_archea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rabbit:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

## Result No. Score Query Match Length DB ID Description

1 144 100.0 180 6 Q951GO 0951g0 canis famili

2 91.7 206 13 Q91410 091410 gallus gallus

3 87.5 204 13 Q12956 heloderma s

4 81.9 220 13 Q8UWL9 08uw19 hopicbarrac

5 79.2 266 13 Q91409 042143 xenopus lae

6 75.7 72 13 Q91409 091409 oncorhynchus

7 75.7 178 13 Q91409 091409 oncorhynchus

8 75.7 178 13 Q91189 091189 oncorhynchus

9 75.7 219 13 Q42144 xenopus lae

10 70.8 160 13 Q9PUR1 09pur1 petromyzon

11 68.1 121 13 Q9DDE6 09dde6 brachydanio

12 66.0 62 13 Q9PRW9 09prw9 scyliorhinus

13 61.1 96 13 Q9DG43 09dg43 amphilophites

14 57.6 120 13 Q9PU00 09pu00 petromyzon

15 59 130 11 Q9CVF1 09cvf1 mus musculus

16 41.0 111 11 Q9d887 09d887 mus musculus

## Database : SPTRMBL\_21;\*

- 1: sp\_archea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rabbit:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archeap:\*

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9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rabbit:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_rvirus:\*

16: sp\_bacteriap:\*

17: sp\_archeap:\*

## Database : SPTRMBL\_21;\*

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DR Proglucagon.

GN PROGLUCAGON.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

Gallus; Gallus.

NCBI\_TAXID=9031;

[1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95205739; PubMed=7776975;

IRW D.M., Wong J.;

RT "trout and chicken proglucagon: alternative splicing generates mRNA transcripts encoding glucagon-like peptide 2.";

RL Mol. Endocrinol. 9:267-277(1995).

DR EMBL: S78477; ARB34506.1; -.

DR HSSP: P01274; ICGN;

DR InterPro: IPR000532; Glucagon.

DR Pfam: PF00123; hormone2; 3.

DR PRINTS: PRO0275; GLUCAGON.

SMART: SM00070; GLUCAGA; 3.

DR PROSITE: PS00260; GLUCAGON; 3.

SO SEQUENCE 206 AA; 23875 MW; AB299E1B02FC6AA4 CRC64;

Query Match 91.7%; Score 132; DB 13; Length 204;

Best Local Similarity 88.9%; Pred. No. 5 1e-12;

Matches 24; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 HAEGTFSDVSYLEGQAKEFIAWLV 27

Db 118 HAEGTFSDVSYLEGQAKEFIAWLV 144

RESULT 3

012956 PRELIMINARY; PRT; 204 AA.

ID 012955 PRELIMINARY; PRT; 204 AA.

AC 012956; 012955;

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE Glucagon precursor.

OS Heloderma suspectum (Gila monster).

OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;

Lepidosaurs; Chordata; Squamata; Anguimorpha; Helodermatidae;

OC Heloderma.

OX NCBI\_TAXID=8554;

RN 1

RP SEQUENCE FROM N.A., ALTERNATIVE SPlicing, AND TISSUE SPECIFICITY.

RC TISSUE-INTESTINE, AND PANCREAS;

RX MEDLINE=9712477; PubMed=9020121;

RA Chen Y.E.; Drucker, D.J.;

RT "issue-specific expression of unique mRNAs that encode proglucagon-derived peptides or exendin 4 in the lizard.";

RL J. Biol. Chem. 272:4108-4115(1997).

CC - FUNCTION: PROMOTES HYDROLYSIS OF GLYCogen AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL (BY SIMILARITY).

CC - ALTERNATIVE PRODUCTS: 2 ISOMERS; LPII (SHOWN HERE) AND LPI; ARE PRODUCED BY ALTERNATIVE SPlicing.

CC - TISSUE SPECIFICITY: ISOMER LPII IS EXPRESSED IN BOTH PANCREAS AND INTESTINE. EXPRESSION OF ISOMER LPI IS RESTRICTED TO THE PANCREAS. NEITHER ISOMER IS DETECTED IN SALIVARY GLAND.

CC - INDUCTION: PRODUCED IN THE CELLS OF THE ISLETS OF LANGHERANS IN PANCREAS, NEITHER ISOMER IS DETECTED IN SALIVARY GLAND.

CC - RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.

CC - SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.

DR EMBL: U77611; ARB31128.1; -.

DR HSP; P01274; ICGN;

DR InterPro: IPR000532; Glucagon.

DR Pfam: PF00123; hormone2; 3.

DR PRINTS: PRO0275; GLUCAGON.

DR SMART: SM00070; GLUCAGA; 3.

DR PROSITE: PS00260; GLUCAGON; 2.

KN Glucagon family; Hormone; Cleavage on pair of basic residues; Signal;

KW Alternative splicing.

FT SIGNAL; 1

FT PEPTIDE; 21

FT PEPTIDE; 53

FT PEPTIDE; 116

FT PEPTIDE; 164

FT VARSPLC; 149

FT VARSPLC; 150

FT VARSPLC; 204

FT VARSPLC; 23553 MW; B132E3FE46873E/2 CRC64;

SO SEQUENCE 204 AA; 23553 MW;

Query Match 87.5%; Score 126; DB 13; Length 204;

Best Local Similarity 85.2%; Pred. No. 4 2e-11;

Matches 23; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 HAEGTFSDVSYLEGQAKEFIAWLV 27

Db 116 HAEGTFSDVSYLEGQAKEFIAWLV 142

RESULT 4

OBWL9 PRELIMINARY; PRT; 220 AA.

ID OBWL9

AC OBWL9;

DT 01-MAR-2002 (TREMBLrel. 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DE proglucagon.

OS Hoplocephalus rugulosus.

OC Hoplocephalus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Neobatrachia; Ranidae;

OC Hoplocephalus.

OX NCBI\_TAXID=11072;

RN [1]

RP SEQUENCE FROM N.A.

RA Young C.-M.; Chow B.-K.C.;

RT Identification of a proglucagon cDNA from Rana tigrina rugulosa that encodes two GLP-1s."

RT Gen. Comp. Endocrinol. 124:0-0(2001).

RL DR EMBL: AF324209; RAL3758.1; -.

DR InterPro: IPR000532; Glucagon.

DR Pfam: PF00123; hormone2; 4.

DR PRINTS: PRO0275; GLUCAGON.

DR SMART: SM00070; GLUCAGA; 4.

DR PROSITE: PS00260; GLUCAGON; UNKNOWN 4.

SO SEQUENCE 220 AA; 25615 MW; C72D926E/F89E381 CRC54;

Query Match 81.9%; Score 118; DB 13; Length 220;

Best Local Similarity 75.0%; Pred. No. 7 5e-10;

Matches 21; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 HAEGTFSDVSYLEGQAKEFIAWLV 28

Db 135 HAEGTFSDVSYLEEKAKEFVDWLK 162

RESULT 5

042143 PRELIMINARY; PRT; 266 AA.

ID 042143

AC 042143;

DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE Glucagon I precursor [Contains: Glucagon; glucagon-like peptide 1A (GLP-1A); glucagon-like peptide 1B (GLP-1B); glucagon-like peptide 1C (GLP-1C); glucagon-like peptide 2 (GLP-2)].

DE xenopus laevis (African clawed frog);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

OC Xenopoda; Xenopus.

OX NCBI\_TAXID=8355;

RN [1]

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPlicing.

RC TISSUE-PANCREAS;



OS Oncorhynchus mykiss (Rainbow trout) (*Salmo gairdneri*).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopercyli; Neopterygi; Teleostei; Euteleostei; Oncorhynchus.  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.  
 RC TISSUE=DISTAL SMALL INTESTINE, AND PANCREAS;  
 RX MEDLINE=95295739; PubMed=7776977;  
 RA Irwin D.M., Wong J.;  
 RT "trout and chicken proglucagon; alternative splicing generates mRNA  
 transcripts encoding glucagon-like peptide 2.";  
 RL Mol. Endocrinol. 9: 267-277(1995).  
 CC -1- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES  
 THE BLOOD SUGAR LEVEL.  
 CC -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.  
 DR EMBL: AF04433; AAB65611.-.  
 DR HSSP: P01274; IGEN.  
 DR InterPro: IPR000532; Glucagon.  
 DR PRINTS: PR00275; GLUCAGON.  
 DR SMART: SM0070; GLUCA; 4.  
 DR PROSITE: PS00260; GLUCAGON; 3.  
 DR GLucagon family; Hormone; Signal; Cleavage on pair of basic residues;  
 KW Multigene family.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT PEPTIDE 53 81 GLUCAGON.  
 FT PEPTIDE 97 133 GLUCAGON-LIKE PEPTIDE 1A.  
 FT PEPTIDE 142 173 GLUCAGON-LIKE PEPTIDE 1B.  
 FT PEPTIDE 180 211 GLUCAGON-LIKE PEPTIDE 1C.  
 SO SEQUENCE 219 AA: 25271 NW; ACC699233C362CEO C064;  
 DR PROSITE: PS00260; GLUCAGON.  
 DR GLucagon family; Hormone; Cleavage on pair of basic residues;  
 KW Glucagon family; Hormone; Cleavage on pair of basic residues; Signal;  
 FT SIGNAL 1 7 POTENTIAL.  
 FT PEPTIDE 49 53 GLUCAGON.  
 FT PEPTIDE 52 80 GLUCAGON-LIKE PEPTIDE 1.  
 FT PEPTIDE 85 120 GLUCAGON-LIKE PEPTIDE 2.  
 FT PEPTIDE 137 169 GLUCAGON-LIKE PEPTIDE 2.  
 FT PEPTIDE 124 178 MISSING (IN PANCREATIC ISOFORM).  
 SQ SEQUENCE 178 AA: 19998 MW; E89D7866CB91C64;  
 Query Match 75.7%; Score 109; DB 13; Length 178;  
 Best Local Similarity 69.2%; Pred. No. 1.4e-08; Indels 0; Gaps 0;  
 Matches 18; Conservative 7; Mismatches 1;  
 PRNTS: PR00275; GLUCAGON.  
 DR SMART: SM00070; GLUCA; 3.  
 DR PROSITE: PS00260; GLUCAGON; UNKNOWN\_2.  
 DR GLucagon family; Hormone; Signal; Cleavage on pair of basic residues;  
 KW Glucagon family; Hormone; Cleavage on pair of basic residues; Signal;  
 FT SIGNAL 1 7 POTENTIAL.  
 FT PEPTIDE 49 53 GRPP (GLUCENTINE RELATED POLYPEPTIDE).  
 FT PEPTIDE 52 80 GLUCAGON.  
 FT PEPTIDE 85 120 GLUCAGON-LIKE PEPTIDE 1.  
 FT PEPTIDE 137 169 GLUCAGON-LIKE PEPTIDE 2.  
 FT PEPTIDE 124 178 MISSING (IN PANCREATIC ISOFORM).  
 SQ SEQUENCE 178 AA: 19998 MW; E89D7866CB91C64;  
 Query Match 75.7%; Score 109; DB 13; Length 178;  
 Best Local Similarity 69.2%; Pred. No. 1.4e-08; Indels 0; Gaps 0;  
 Matches 18; Conservative 7; Mismatches 1;  
 PRNTS: PR00275; GLUCAGON.  
 DR SMART: SM00070; GLUCA; 3.  
 DR PROSITE: PS00260; GLUCAGON.  
 DR GLucagon family; Hormone; Signal; Cleavage on pair of basic residues;  
 KW Glucagon family; Hormone; Signal; Cleavage on pair of basic residues;  
 FT SIGNAL 1 7 POTENTIAL.  
 FT PEPTIDE 49 53 GLUCAGON.  
 FT PEPTIDE 52 80 GLUCAGON.  
 FT PEPTIDE 85 120 GLUCAGON-LIKE PEPTIDE 1.  
 FT PEPTIDE 137 169 GLUCAGON-LIKE PEPTIDE 2.  
 FT PEPTIDE 124 178 MISSING (IN PANCREATIC ISOFORM).  
 SQ SEQUENCE 178 AA: 19998 MW; E89D7866CB91C64;  
 Query Match 75.7%; Score 109; DB 13; Length 178;  
 Best Local Similarity 69.2%; Pred. No. 1.4e-08; Indels 0; Gaps 0;  
 Matches 18; Conservative 7; Mismatches 1;  
 PRNTS: PR00275; GLUCAGON.  
 DR SMART: SM00070; GLUCA; 3.  
 DR PROSITE: PS00260; GLUCAGON.  
 DR GLucagon family; Hormone; Signal; Cleavage on pair of basic residues;  
 KW Glucagon family; Hormone; Signal; Cleavage on pair of basic residues;  
 FT SIGNAL 1 22 POTENTIAL.  
 FT PEPTIDE 43 71 GLUCAGON.  
 FT PEPTIDE 82 113 GLUCAGON-LIKE PEPTIDE 1.  
 FT PEPTIDE 130 160 GLUCAGON-LIKE PEPTIDE 2.

RESULT 9

O4144 PRELIMINARY; PRT; 219 AA.

ID O42144 PRELIMINARY; PRT; 219 AA.

AC DT 01-JAN-1998 (TREMBLER, 05, Created)  
 DT 01-JUN-1998 (TREMBLER, 05, Last sequence update)  
 DT 01-JUN-2001 (TREMBLER, 17, Last annotation update)

DE Glucagon I precursor [Contains: Glucagon; glucagon-like peptide 1 (GLP-1); glucagon-like peptide 2 (GLP-2)].  
 OS Petromyzon marinus (Sea lamprey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.  
 NCBI\_TaxID=7757;

RN [1] SEQUENCE FROM N.A.  
 RP TISSUE=INTESTINE;  
 RC MEDLINE=94010172; PubMed=10555286;  
 RA Irwin D.M., Huner O., Youson J.H.;  
 RT "Lamprey proglucagon and the origin of glucagon-like peptides.";  
 RL Mol. Biol. Evol. 16:1548-1557(1999).

RN [2] SEQUENCE OF 43-71 AND 82-113.  
 RP TISSUE=INTESTINE;  
 RC MEDLINE=94010172; PubMed=8405897;  
 RA Conlon J.M., Nielsen P.F., Youson J.H.;  
 RT "Primary structures of glucagon and glucagon-like peptide isolated from the intestine of the parasitic lamprey Petromyzon marinus.";  
 RT Gen. Comp. Endocrinol. 91:96-104(1993).  
 CC -1- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.  
 CC -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.  
 DR EMBL: AF159707; AAF09186.1.-.  
 DR HSSP: P01275; IBB0.  
 DR InterPro: IPR000532; Glucagon.  
 DR PRINTS: PR00123; hormone2; 2.  
 DR SMART: SM00070; GLUCAGON.  
 DR PROSITE: PS00260; GLUCAGON; 2.  
 DR GLucagon family; Hormone; Signal; Cleavage on pair of basic residues;  
 KW Multigene family.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT PEPTIDE 43 71 GLUCAGON.  
 FT PEPTIDE 82 113 GLUCAGON-LIKE PEPTIDE 1.  
 FT PEPTIDE 130 160 GLUCAGON-LIKE PEPTIDE 2.

RN [1] SEQUENCE FROM N.A.  
 RP TISSUE= PANCREAS;  
 RC MEDLINE=97365292; PubMed=9223287;  
 RA Irwin D.M., Satkunarajah M., Wen Y., Brubaker P.L., Pederson R.A., Wheeler M.B.;  
 RT "The Xenopus proglucagon gene encodes novel GLP-1-like peptides with insulinotropic properties.";  
 RT proc. Natl. Acad. Sci. U.S.A. 94:7915-7920(1997).  
 RL



DT 01-MAY-2000 (TREMBrel. 13, Created)  
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)  
 DE Glucagon II precursor [Contains: Glucagon; glucagon-like peptide (GLP)].  
 OS Petromyzon marinus (Sea lamprey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.  
 RN [1]  
 RP  
 RC TISSUE=INTESTINE;  
 RX MEDLINE=20022986; Pubmed=10355286;  
 RA Irwin D.M., Huner O., Youson J.H.  
 RT "Lamprey proglucagon and the origin of glucagon-like peptides.";  
 RL Mol. Biol. Evol. 16:1548-1557(1999).  
 CC -I FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES THE BLOOD SUGAR LEVEL.  
 CC -I SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.  
 DR EMBL; AF159708; AF091871; .  
 DR HSSP; P01275; 1BHO.  
 DR InterPro; IPR000532; Glucagon.  
 DR Pfam; PF00123; hormone2; 1.  
 DR PRINTS; PR0075; GLUCAGON.  
 DR SMART; SM00070; GLUCA; 2.  
 DR PROSITE; PS00260; GLUCAGON; 2.  
 KW Glucagon family; Hormone; Signal; Cleavage on pair of basic residues;  
 KW Multigene family.  
 FT SIGNAL 1 ? POTENTIAL.  
 FT PEPTIDE 44 72 GLUCAGON-LIKE PEPTIDE.  
 FT PEPTIDE 89 120 AA; 13397 MN; FBDE667B96E198DB CRC64;  
 SEQUENCE 120 AA: 13397 MN; FBDE667B96E198DB CRC64;

Query Match 57.6%; Score 83; DB 13; Length 120;  
 Best Local Similarity 48.1%; Pred. No. 8.1e-05; Mismatches 5; Indels 0; Gaps 0;  
 Matches 13; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 HAGCTFTSDVSSYLEGQAKEFFIAWLW 27  
 |:|:||||| |:|:|||:|||:  
 Db 1 44 HSGCFSFTSDYSKILDVKOAKDFVNWLL 70

RESULT 15

09CVF1 PRELIMINARY; PRT: 130 AA.

ID 09CVF1  
 AC 09CVF1;  
 DT 01-JUN-2001 (TREMBrel. 17, Created)  
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)  
 DE 01-DEC-2001 (TREMBrel. 19, Last annotation update)  
 DE Gastric inhibitory polypeptide (Fragment).  
 GN GIP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus. NCBI\_TAXID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=57BL/6J; TISSUE=SMALL INTESTINE;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Kohno H., Kadoch J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kodota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido R., Furuno M., Aono H., Baldarelli R., Barish G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hume D.A., Kamoya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N., RA

RA Sasaki H., Sato K., Schoenbach C., Seiya T., Shibusawa Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynnshaw-Boriss A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., RA Hayashizaki Y., Functional annotation of a full-length mouse cDNA collection. " Nature 409:685-690(2001).  
 RL Nature 409:685-690(2001).  
 DR EMBL; ARK008325; BAB25720.1; -. DR HSSP; P01274; 1GCN.  
 DR MGDB; MGJ:101504; Gip.  
 DR InterPro; IPR000532; Glucagon.  
 DR Pfam; PF00123; hormone2; 1.  
 DR SMART; SM00070; GLUCA; 1.  
 DR PROSITE; PS00260; GLUCAGON; 1.  
 FT NON-TER 1 14906 MN; 95B3B6E91E2A7992 CRC64;  
 SQ SEQUENCE 130 AA: 14906 MN; 95B3B6E91E2A7992 CRC64;

Query	Match	Best Local Similarity	Score	DB	Length
QY	1 HAGCTFTSDVSSYLEGQAKEFFIAWLW 27	41.0%	59	11	130
Db	30 YAGCTFISDYSIAMDKIROQDFVNWL 56	40.7%	27	7	111

Search completed: March 19, 2003, 12:11:33  
 Job time : 31 secs